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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:36:38 ; Search time 48.9541 Seconds
(without alignments)
249.264 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964

Sequence: 1 MLOMAGCQSQNEFYDSLHA.....CKSLPAALSATBIKXSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-------|---------------------|
| 1 | 964 | 100.0 | 184 | 4 | US-09-565-423-11 |
| 2 | 950 | 98.5 | 181 | 4 | US-09-854-864-5 |
| 3 | 572 | 59.3 | 185 | 4 | US-09-565-423-17 |
| 4 | 572 | 59.3 | 185 | 4 | US-09-854-864-11 |
| 5 | 323 | 33.5 | 58 | 4 | US-09-854-864-21 |
| 6 | 311.5 | 32.3 | 117 | 4 | US-09-854-864-12 |
| 7 | 286 | 29.7 | 283 | 4 | US-09-854-864-9 |
| 8 | 284 | 29.5 | 51 | 4 | US-09-854-864-6 |
| 9 | 201 | 20.9 | 34 | 4 | US-09-854-864-7 |
| 10 | 201 | 20.9 | 81 | 4 | US-09-854-864-13 |
| 11 | 187 | 19.4 | 281 | 4 | US-09-854-864-10 |
| 12 | 104 | 10.8 | 21 | 4 | US-09-854-864-8 |
| 13 | 79.5 | 8.2 | 1009 | 2 | US-08-357-642A-1 |
| 14 | 79.5 | 8.2 | 1009 | 2 | US-08-460-626-1 |
| 15 | 78.5 | 8.1 | 293 | 2 | US-08-810-572A-2 |
| 16 | 78.5 | 8.1 | 293 | 3 | US-09-230-333-2 |
| 17 | 78.5 | 8.1 | 293 | 4 | US-09-782-857A-2 |
| 18 | 78.5 | 8.1 | 293 | 4 | US-09-879-919-22 |
| 19 | 78.5 | 8.1 | 293 | 4 | US-09-848-295-4 |
| 20 | 78.5 | 8.1 | 293 | 4 | US-09-854-864-14 |
| 21 | 76 | 7.9 | 744 | 1 | US-08-179-481F-2 |
| 22 | 75 | 7.8 | 857 | 1 | US-07-717-331F-2 |
| 23 | 73.5 | 7.6 | 307 | 4 | US-09-583-110-2671 |
| 24 | 71.5 | 7.4 | 835 | 4 | US-09-489-019A-8740 |
| 25 | 71 | 7.4 | 333 | 4 | US-09-328-352-6022 |
| 26 | 70.5 | 7.3 | 154 | 3 | US-09-232-160-18 |
| 27 | 70.5 | 7.3 | 397 | 4 | US-09-854-864-18 |

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|-----|------|-----|------|---|----------------------|--------------------|
| 28 | 70 | 7.3 | 180 | 4 | US-09-780-717-11 | Sequence 11, Appl |
| 29 | 70 | 7.3 | 182 | 4 | US-09-780-717-44 | Sequence 44, Appl |
| 30 | 69.5 | 7.2 | 59 | 4 | US-09-854-864-20 | Sequence 20, Appl |
| 31 | 69.5 | 7.2 | 166 | 3 | US-08-810-572A-6 | Sequence 6, Appl |
| 32 | 69.5 | 7.2 | 166 | 3 | US-09-290-333-6 | Sequence 6, Appl |
| 33 | 69.5 | 7.2 | 166 | 4 | US-09-782-857A-6 | Sequence 6, Appl |
| 34 | 69.5 | 7.2 | 166 | 4 | US-09-854-864-15 | Sequence 15, Appl |
| 35 | 69.5 | 7.2 | 217 | 4 | US-09-252-991A-30641 | Sequence 30641, A |
| 36 | 69.5 | 7.2 | 224 | 4 | US-09-465-901-30 | Sequence 30, Appl |
| 37 | 69.5 | 7.2 | 353 | 4 | US-09-328-352-5429 | Sequence 5429, Ap |
| 38 | 69.5 | 7.2 | 942 | 4 | US-09-695-481-2 | Sequence 2, Appl |
| 39 | 69.5 | 7.2 | 1043 | 4 | US-09-695-481-6 | Sequence 6, Appl |
| 40 | 69.5 | 7.2 | 1180 | 3 | US-08-560-148-2 | Sequence 2, Appl |
| 41 | 69.5 | 7.2 | 1212 | 3 | US-08-660-148-5 | Sequence 5, Appl |
| 42 | 69.5 | 7.2 | 1212 | 4 | US-09-695-481-7 | Sequence 7, Appl |
| 43 | 69.5 | 7.2 | 1706 | 2 | US-08-459-568-2 | Sequence 2, Appl |
| 44 | 69.5 | 7.2 | 1706 | 2 | US-08-399-411-2 | Sequence 2, Appl |
| 45 | 69.5 | 7.2 | 1706 | 3 | US-08-516-859A-2 | Sequence 2, Appl |
| 46 | 69.5 | 7.2 | 1706 | 3 | US-09-586-472-2 | Sequence 2, Appl |
| 47 | 69.5 | 7.2 | 1706 | 4 | US-09-528-706-2 | Sequence 2, Appl |
| 48 | 69.5 | 7.2 | 2496 | 3 | US-09-125-028-2 | Sequence 2, Appl |
| 49 | 69.5 | 7.2 | 2958 | 3 | US-08-894-344C-2 | Sequence 2, Appl |
| 50 | 69 | 7.2 | 324 | 2 | US-08-579-940-7 | Sequence 7, Appl |
| 51 | 69 | 7.2 | 445 | 1 | US-08-353-400-33 | Sequence 33, Appl |
| 52 | 69 | 7.2 | 447 | 6 | 5455030-1 | Patent No. 5455030 |
| 53 | 69 | 7.2 | 464 | 1 | US-08-353-400-36 | Sequence 36, Appl |
| 54 | 69 | 7.2 | 599 | 1 | US-08-442-542-18 | Sequence 18, Appl |
| 55 | 69 | 7.2 | 599 | 3 | US-08-765-469-18 | Sequence 18, Appl |
| 56 | 68.5 | 7.1 | 228 | 4 | US-09-107-532A-3896 | Sequence 3896, Ap |
| 57 | 68.5 | 7.1 | 235 | 3 | US-08-651-136C-8 | Sequence 8, Appl |
| 58 | 68.5 | 7.1 | 235 | 3 | US-09-229-911A-8 | Sequence 8, Appl |
| 59 | 68.5 | 7.1 | 409 | 4 | US-09-538-092-1214 | Sequence 1214, Ap |
| 60 | 68.5 | 7.1 | 877 | 1 | US-08-072-574-12 | Sequence 12, Appl |
| 61 | 68.5 | 7.1 | 877 | 1 | US-08-486-270-12 | Sequence 12, Appl |
| 62 | 68.5 | 7.1 | 877 | 3 | US-08-367-264-12 | Sequence 12, Appl |
| 63 | 68.5 | 7.1 | 877 | 3 | US-09-153-757-12 | Sequence 12, Appl |
| 64 | 68.5 | 7.1 | 877 | 4 | US-09-459-715-12 | Sequence 12, Appl |
| 65 | 68.5 | 7.1 | 1180 | 1 | US-08-072-574-8 | Sequence 8, Appl |
| 66 | 68.5 | 7.1 | 1180 | 1 | US-08-486-270-8 | Sequence 8, Appl |
| 67 | 68.5 | 7.1 | 1180 | 3 | US-08-367-264-8 | Sequence 8, Appl |
| 68 | 68.5 | 7.1 | 1180 | 4 | US-09-153-757-8 | Sequence 8, Appl |
| 69 | 68.5 | 7.1 | 1180 | 4 | US-09-459-715-8 | Sequence 8, Appl |
| 70 | 68.5 | 7.1 | 1212 | 1 | US-08-072-574-10 | Sequence 10, Appl |
| 71 | 68.5 | 7.1 | 1212 | 1 | US-08-486-270-10 | Sequence 10, Appl |
| 72 | 68.5 | 7.1 | 1212 | 3 | US-08-367-264-10 | Sequence 10, Appl |
| 73 | 68.5 | 7.1 | 1212 | 4 | US-09-153-757-10 | Sequence 10, Appl |
| 74 | 68.5 | 7.1 | 1212 | 4 | US-09-459-715-10 | Sequence 10, Appl |
| 75 | 68 | 7.1 | 317 | 2 | US-08-466-337A-18 | Sequence 18, Appl |
| 76 | 68 | 7.1 | 317 | 2 | US-08-475-359-18 | Sequence 18, Appl |
| 77 | 68 | 7.1 | 317 | 3 | US-08-465-887A-18 | Sequence 18, Appl |
| 78 | 67.5 | 7.0 | 178 | 1 | US-08-825-891-1 | Sequence 1, Appl |
| 79 | 67.5 | 7.0 | 297 | 4 | US-09-548-130-6 | Sequence 6, Appl |
| 80 | 67.5 | 7.0 | 799 | 1 | US-08-188-228-42 | Sequence 42, Appl |
| 81 | 67.5 | 7.0 | 799 | 1 | US-08-332-638-42 | Sequence 42, Appl |
| 82 | 67 | 7.0 | 182 | 3 | US-09-045-632-29 | Sequence 29, Appl |
| 83 | 67 | 7.0 | 283 | 3 | US-09-045-632-27 | Sequence 27, Appl |
| 84 | 67 | 7.0 | 310 | 3 | US-08-651-136C-22 | Sequence 22, Appl |
| 85 | 67 | 7.0 | 310 | 3 | US-09-329-911A-22 | Sequence 22, Appl |
| 86 | 67 | 7.0 | 320 | 2 | US-08-579-940-8 | Sequence 8, Appl |
| 87 | 67 | 7.0 | 489 | 4 | US-08-190-204-2 | Sequence 2, Appl |
| 88 | 67 | 7.0 | 489 | 5 | PCT-US93-11110-1 | Sequence 1, Appl |
| 89 | 67 | 7.0 | 498 | 6 | 5221789-1 | Patent No. 5221789 |
| 90 | 67 | 7.0 | 498 | 3 | US-09-045-632-30 | Sequence 30, Appl |
| 91 | 67 | 7.0 | 502 | 3 | US-09-045-632-24 | Sequence 24, Appl |
| 92 | 67 | 7.0 | 502 | 3 | US-09-045-632-36 | Sequence 36, Appl |
| 93 | 67 | 7.0 | 599 | 3 | US-09-045-632-28 | Sequence 28, Appl |
| 94 | 67 | 7.0 | 602 | 3 | US-09-045-632-20 | Sequence 20, Appl |
| 95 | 67 | 7.0 | 609 | 2 | US-08-716-301-4 | Sequence 4, Appl |
| 96 | 67 | 7.0 | 642 | 3 | US-09-045-632-35 | Sequence 35, Appl |
| 97 | 67 | 7.0 | 702 | 3 | US-09-045-632-15 | Sequence 15, Appl |
| 98 | 67 | 7.0 | 818 | 3 | US-09-045-632-25 | Sequence 25, Appl |
| 99 | 67 | 7.0 | 861 | 3 | US-09-045-632-34 | Sequence 34, Appl |
| 100 | 67 | 7.0 | 918 | 3 | US-09-045-632-21 | Sequence 21, Appl |

ALIGNMENTS

RESULT 1

US-09-565-423-11

; Sequence 11, Application US/09565423

; Patent No. 6475987

; GENERAL INFORMATION:

; APPLICANT: SHU, HONG-BING

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/09/565,423

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO. 11

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-565-423-11

Query Match 100.0%; Score 964; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 9.8e-104;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60

Db 1 MLAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLE 120

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLE 120

Qy 121 YVTECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180

Db 121 YVTECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184

Db 181 ISAR 184

RESULT 2

US-09-854-864-5

; Sequence 5, Application US/09854864

; Patent No. 6774106

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: BLYS/AGP-3, AND TACI

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-5

Query Match 98.5%; Score 950; DB 4; Length 181;

Best Local Similarity 100.0%; Pred. No. 4e-102;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCLGSL 63

Db 1 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCLGSL 60

Qy 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 123

Db 61 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 120

Qy 124 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKSISA 183

Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKSISA 180

Qy 184 R 184

Db 181 R 181

RESULT 3

US-09-565-423-17

; Sequence 17, Application US/09565423

; Patent No. 6475987

; GENERAL INFORMATION:

; APPLICANT: SHU, HONG-BING

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/09/565,423

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-565-423-17

Query Match 59.3%; Score 572; DB 4; Length 185;

Best Local Similarity 62.6%; Pred. No. 3.1e-58;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

Qy 4 MAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCORYCNASVTNSVKGNTNAILWTCLGSL 63

Db 1 MAQCFFHSEYFDSLHACKFCHLRCSN--PPATCQPCDPSVTSSVKGTVTLWIFLGLT 58

Qy 64 LIISLAVFVLMFLLRKISSEPLKDEFKN---TGSLGGMANIDLEKSRGTDEIILPRGL 119

Db 59 LVLSLALFTISFLRKNNPEALKDEPQSQQLDGSQQLDKADTELTRIRAGDDRIFPRSL 118

Qy 120 EYVTECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCK-SLPAAL-SATEI 177

Db 119 EYVTECTCEDCVKSPKGDSDHFFPLPAMEGATILVTTKTDYCKSGSVPTALQSVGM 178

Qy 178 EKSISAR 184

Db 179 EKPTHTR 185

RESULT 4

US-09-854-864-11

; Sequence 11, Application US/09854864

; Patent No. 6774106

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

Db 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34

RESULT 10
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
; US-09-854-864-13

Query Match 20.9%; Score 201; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 41
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Db 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34
|||||

RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-854-864-10

Query Match 19.4%; Score 187; DB 4; Length 281;
Best Local Similarity 29.8%; Pred. No. 2.7e-13;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;

QY 4 MAQCQSQNEYFDSLHACIPCOLRCSNTPLTCQRYCNASVTNSVKGTTAILWTCLGLS 63
|||||
Db 1 MAQCQPSHEYFDSLHACKPCHLRCSN--PPATCQPCYCDPVSSTSVKGS----- 47
|||||

QY 64 LIISLAVFLVLMFLLRKISSEPLKDFKNTGSG-----LLGMANIDLEKSR 108
|||||

Db 48 -----YTGGGGDKTHTCCPAPALGCPVSFLLPPK 80

QY 109 TGDTEILPRLGLEYTVECTEDCIKSPKVDSD-----HCFPLPAMBE-----GAT 154

Db 81 PKDTLMSRTEVTVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 137
Qy 155 ILVTTKNDY-----CKSLPAALSATEIEKTS 182
Db 138 SVLTVLHQDWLNGKEYKCKVSNKALPAP-PIEKTIS 171

RESULT 12
US-09-854-864-8
; Sequence 8, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-8

Query Match 10.8%; Score 104; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ILWTCGLGLSLIISLAVFLVLMF 75
Db 1 ILWTCGLGLSLIISLAVFLVLMF 21

RESULT 13
US-08-357-642A-1
; Sequence 1, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: FYK2 RELATED PRODUCTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 211/121
; REFERENCE/DOCKET NUMBER: 32,327
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single

; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-357-642A-1

Query Match 8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

Qy 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEVTVECTCSDCIKSPKV 138
Db 249 KFFNT---LAGFANIDQETVRCELIQGNWITVDLVIGPKGIRQLTSDAKPTCLAEFKQI 305

Qy 139 DSDHCPLPAMERGATIL 156
Db 306 RSIRCLPL---ERQAVL 320

RESULT 14
US-08-460-626-1
; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
; APPLICANT: SIMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: FYK-2 RELATED PRODUCTS AND
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-626-1

Query Match 8.1%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

QY 88 EFKTSGGLGMANIDLEKSR-----TGDEILLPRGLYTVETCTEDCIKSPKV 138
DB 249 KFFNT--LAGFANIDQETVRCELIQGNITVDLVIGKGIQLTSDAKPTCLAEFKQI 305

QY 139 DSDHCFPLPAMEGATIL 156
DB 306 RSRCLFL---EEQAVL 320

RESULT 15
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 8.1%; Score 78.5; DB 2; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEYFDSLHACIPQLCRSSNTPPLTCQRYCNASVTSVKGT--NAILWTCLGLSLI 65
DB 34 CPEQYWDPLLTGTCMCKTICNHQS-ORTCAAFCSLSCKRQKGFYDHLRLDCISCASI 92

QY 66 I-----SLAVFVLMFL-----LRKISSEPLKDFKNTGSGLLGMANIDLEKS----- 107
DB 93 CGQHPKQCAFCENKLRSPVNLPPELRRQSRGSEVENNSDNGR-YQGLEHRSSEASPALP 151

QY 108 ---RTGDEILLPRG-----LEVTVECTCEDCIKSP-----KVD 139
DB 152 GLKLSADQVALVYSTGLCLCAVLCLVAVACFLKRGDPCSCQP--RSRPRQSPAKSS 209

QY 140 SDHCFPLPAMEGATILVTTKTNDYC 165
DB 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 16
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 8.1%; Score 78.5; DB 3; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEYFDSLHACIPQLCRSSNTPPLTCQRYCNASVTSVKGT--NAILWTCLGLSLI 65
DB 34 CPEQYWDPLLTGTCMCKTICNHQS-ORTCAAFCSLSCKRQKGFYDHLRLDCISCASI 92

QY 66 I-----SLAVFVLMFL-----LRKISSEPLKDFKNTGSGLLGMANIDLEKS----- 107
DB 93 CGQHPKQCAFCENKLRSPVNLPPELRRQSRGSEVENNSDNGR-YQGLEHRSSEASPALP 151

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Qy 108 ---RTGDEIILPRG-----LVTVECTCEDCIKSP-----KVD 139
Db 152 GUKLSADQVALVYLTGLCLCAVLCFLKKRGDPSCQP--RSRQSPAKSS 209
Qy 140 SDHCFPLPAMEEGATILVTTKINDYC 165
Db 210 ODH-----AMEAGSPVSTSPRPVETC 230

```

RESULT 17
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF

```

QY 108 ----RTGBEILPRG-----LEYTVSECTCEDCICKSP-----KVD 139
      :|:|:|
DB 152 GLKLSADOALVSTLGLCLCAVLCCFLVAVACFKKRGDPCSCQP---RSRPROSPAKSS 209
      :|:|:|
QY 140 SDHCFFLPAMEEGATILVTTTKTNDYC 165
      |||:|:|:|
DB 210 ODH-----AMEAGSPVSTSPPEPVTC 230
      |||:|:|:|

```

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RESULT 18
US-09-879-919-22
/ Sequence 22, Application US/09879919
/ Patent No. 6541224
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Guo-Liang, et al.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
/ FILE REFERENCE: PF253P1
/ CURRENT APPLICATION NUMBER: US/09/879,919
/ CURRENT FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/016,812
/ PRIOR FILING DATE: 1996-03-14
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-879-919-22

```

[illegible]

RESULT 19
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based

GENERAL INFORMATION:
 APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
 APPLICANT: Stein
 TITLE OF INVENTION: A Receptor Protein Kinase Gene
 TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Yahwak & Associates
 STREET: 25 Skytop Drive
 CITY: Trumbull
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06611
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/717,331P
 FILING DATE: June 19th 1991
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: George M. Yahwak
 REGISTRATION NUMBER: 26,824
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203)268-1951
 TELEFAX: (203)268-1951
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 857 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-717-331P-2

Query Match 7.8%; Score 75; DB 1; Length 857;
 Best Local Similarity 17.6%; Pred. No. 13;
 Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

QY 24 COLRCSNTPPLTCQRYCNASVTSVKGTTNAILMT-----58
 DB 380 CKKRCISD--CNCTAFANADIRNG--GSGCVIWTTERLEDIRNYATDAIDGQDLYVRLAA 434
 QY 59 -----CGLSLTISLAVFLMFLRKISSEPLKDEPKNTGSGLLGMANIDLEK 106
 DB 435 ADIAKKNASGKIISLTGVSVLLIMFCL-----WKKKQKRAKASAIISINTORNO 487
 QY 107 SRTGDEIILPRGLETVVEECTCEDCIKSPKVDSDHCF-----PLPAMEGATILVTTKT 161
 DB 488 NLPNMVU-----SSKRFSGEYKFEELPLIEME---TVVKATEN 527
 QY 162 NDYCKSL 169
 DB 528 FSSCNKL 534

RESULT 23
 US-09-583-110-2671
 Sequence 2671, Application US/09583110
 Patent No. 6699703
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 FILE REFERENCE: PATH00-07A
 CURRENT APPLICATION NUMBER: US/09/583,110
 CURRENT FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/107,433
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/085,131
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO 2671
 LENGTH: 307
 TYPE: PRT
 ORGANISM: Streptococcus pneumoniae
 US-09-583-110-2671

Query Match 7.6%; Score 73.5; DB 4; Length 307;
 Best Local Similarity 26.2%; Pred. No. 4.5;
 Matches 48; Conservative 26; Mismatches 60; Indels 49; Gaps 12;

QY 1 MLQWAGQCSQNEYFDSLHACIFCOLRCSNTPPLTCQRYCN-ASVTSVK-GTNAILWT 58
 DB 1 MTELAKQLLE-----LTYIVIGCQFLHTA-----YCSYKDKTNPVRLGTSF-FWT 44
 QY 59 CGLSLI-----ISLAVFLMFLRL-----KISSEPLKDEPKNTGSGLLGMANIDLE 105
 DB 45 LLSITFIGGSMYPMNSIGIIVILLSLTLFKQVRIGTLPISLDEWK-----ANI--E 93
 QY 106 KSRTGDEIILPRGLETVVEECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYC 165
 DB 94 SNRLKKNKIFIPVML-MAILALVLAQMIPFSKIS-----ISLAL--FATISVLVITNSHP 146
 QY 166 KSL 168
 DB 147 KSL 149

RESULT 24
 US-09-489-039A-8740
 Sequence 8740, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 8740
 LENGTH: 835
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-8740

Query Match 7.4%; Score 71.5; DB 4; Length 835;
 Best Local Similarity 21.0%; Pred. No. 32;
 Matches 56; Conservative 36; Mismatches 80; Indels 95; Gaps 14;

QY 1 MLQWAGQCSQNE-----YFDSLHACIP---COL-----RCSNTPPLT 36
 DB 199 MILMAGFTAGNEKGLVILGRNGSDYSAVAALACLRADCCCEIWTVDGVVTCDPQVPP-- 256
 QY 37 CORYCNASVTSVKGTTNAILWTCLGLSL-----IISLAVFLMFLRLKISSEPL----- 85
 DB 257 -----DARLLKSMYSQEMELSYFGAKVLPHTPIAQFOIPLCKIKNTGNPQAPGTLIG 311
 QY 86 --KDE-----FKNTGSGLLGM-----ANIDLEKSRGTDEIIL--PRGLE 121
 DB 312 ASRDEDDLPLVKISNLNNMAMFNVSFGMKGMVMAARVATMSRAGISVVLVITQSSEY 371
 QY 122 TVBEECTCE-DCIKSPKVDSDHCF-----PLPAMEGATILVTTKTNDYCKSLP--- 169
 DB 372 SISFCVPQSDCARAKRAMEDEFYLEKGLLEPLAIMERLAIISV---VGDGMFTLRGIS 428
 QY 170 ----AALSATEI-----EKSIS 182
 DB 429 AKFFAALARANINIVAIAQSSERSIS 455

RESULT 25

US-09-328-352-6022

; Sequence 6022, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 6022

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-6022

Query Match 7.4%; Score 71; DB 4; Length 333;

Best Local Similarity 24.7%; Pred. No. 9.9;

Matches 36; Conservative 29; Mismatches 67; Indels 14; Gaps 6;

Qy 45 VTNVSGTNAI-LWTCIGLSLIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANI- 102

Db 6 ISNKEQGTLLIELIVALALGLIL-VAATAQLFIGLLSSRLQKANAELQDSGIFGLETMA 64

Qy 103 -DLEKSRGTDEILPR-----GLEVTVEECTCEDCIKSPKYVSDHCFPLPAMEGA 153

Db 65 RDILRLNYGN-VVNPQLDTTTPWGGIVLTGSTATNANNINFIKVDITNTYIPEALLSRGA 123

Qy 154 TILVTTKTNDYCKSLPAALSATEIEK 179

Db 124 GDTVST-VNNHWKGLSNQNSSNAEE 148

RESULT 26

US-09-232-160-18

; Sequence 18, Application US/09232160

; Patent No. 6368794

; GENERAL INFORMATION:

; APPLICANT: Steve Daniel

; APPLICANT: James Gilmore

; APPLICANT: Susan G. Stuart

; APPLICANT: Laura Stuve

; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL

; FILE REFERENCE: PA-0003 US

; CURRENT APPLICATION NUMBER: US/09/232,160

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PERL Program

; SEQ ID NO 18

; LENGTH: 154

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: -

; OTHER INFORMATION: 1299627

US-09-232-160-18

Query Match 7.3%; Score 70.5; DB 3; Length 154;

Best Local Similarity 25.2%; Pred. No. 3.7;

Matches 30; Conservative 16; Mismatches 52; Indels 21; Gaps 6;

Qy 13 YFDSLHLAC-IPQLRCSSNTPLTCQRYCNASVTNSVKGTTNAILWTCIG---LSLIIS 67

Db 23 YADDCLAQCKGCKSYCCDGTTPYCCSY--AVIGNILSGT-AIAGIVFGIVFMGVIA 79

Qy 68 LAVFVLMFLRKISSEPLKDFKNTGSGLLGMANTDLEKSRGTGDSIIILPRGLETVTEEC 126

Db 80 IATICQWCM-----KNHRATRVGLTRTTHINTVSSYPGPP---PYGHDHEMEYC 125

```
Db 76 ATYNINWYISNKLLOEKGDPP-----A 97
Qy 129 EDCIKSKPKVDSDHCFPLPAMEEGATILVTKTNDYCKS---LPAALSAT 175
Db 98 EACLKDCHELVS-----AIPELKDVLDDFKDKDYKANIELSAAMEAS 141

RESULT 29
US-09-780-717-44
; Sequence 44, Application US/09780717
; Patent No. 6713666
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Tim
; APPLICANT: Bates, Nic
; APPLICANT: Allen, Stephen M.
; TITLE OF INVENTION: No. 6713666el Invertase Inhibitors and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 035718/208677
; CURRENT APPLICATION NUMBER: US/09/780,717
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,509
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Glycine max
US-09-780-717-44

Query Match 7.3%; Score 70; DB 4; Length 182;
Best Local Similarity 24.8%; Pred. No. 5.4;
Matches 27; Conservative 23; Mismatches 51; Indels 8; Gaps 2;

Qy 77 LRKISSPLKDEFFKNTGSLGGMANIDLEKSRGTGDEI--ILPRGLEVTVECTEDCIKS 134
Db 53 IQYLSDDPRSTEADVTGLALIMVNIKANNALDKIHLQKNPEPSQKEPLSSCAARY 112
Qy 135 KPKVDSDHCFPLPAMEEGATILVTKTNDYCKSLPAALSATEIEKSISA 183
Db 113 KAIYEAQVAQVASLQKQDPKFAEDGAND-----NAIEATTGNSPSA 155

RESULT 30
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match 7.2%; Score 69.5; DB 4; Length 59;
Best Local Similarity 25.0%; Pred. No. 1.2;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGT--NAILWTCIGLSLI 65
```

```
Db 1 CPBEQYWDPLLTGCMSCCTICNHQS-QRTCAAFCRSLSCRKEQKQFYDHLRLDCISCASI 59

RESULT 31
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 7.2%; Score 69.5; DB 2; Length 166;
Best Local Similarity 25.0%; Pred. No. 5.4;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGT--NAILWTCIGLSLI 65
Db 34 CPBEQYWDPLLTGCMSCCTICNHQS-QRTCAAFCRSLSCRKEQKQFYDHLRLDCISCASI 92

RESULT 32
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

FILING DATE: 14-Feb-2001

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30641
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30641

Query Match 7.2%; Score 69.5; DB 4; Length 217;
Best Local Similarity 25.7%; Pred. No. 8;
Matches 29; Conservative 11; Mismatches 46; Indels 27; Gaps 4;
QY 22 IPCQLRCSNTPPLTCQRYCNASVTSVKGNTNAILWTCLGLSLIISLAVFVLMFLLRKIS 81
DB 124 INCPNASFSQTPAWVCWSSCSRSITQVPGNSLIL---VG-----A 161
QY 82 SEPLKDFKNTGS-----GLLGMANIDLEKSRGTGDEILLPRGLEVTVECTCED 130
DB 162 REPITITTCSTGSAASAGAENAKRDRESARGAKGMRGMR-RFPSCCFD 213

RESULT 36

US-09-465-901-30

; Sequence 30, Application US/09465901

; Patent No. 6492143

; GENERAL INFORMATION:

; APPLICANT: Reed, Randall

; APPLICANT: Yau, King-Wai

; APPLICANT: Krautwurst, Dietmar

; TITLE OF INVENTION: Olfactory Receptor Expression Libraries

; FILE REFERENCE: 001107.00105

; CURRENT APPLICATION NUMBER: US/09/465,901

; CURRENT FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: 60/112,605

; PRIOR FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 224

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; OTHER INFORMATION: PCR primer

US-09-465-901-30

Query Match 7.2%; Score 69.5; DB 4; Length 224;
Best Local Similarity 26.4%; Pred. No. 8.4;
Matches 34; Conservative 16; Mismatches 50; Indels 29; Gaps 7;

QY 8 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTSVKGNTNAILWTCLGLSLII 66
DB 106 CGPNEIHFTCH-----VPLP-LKLACGENVLEKAGVGVICITALLGCFLLI 152
QY 67 SLA-VFVLMFLLRKISSEPLKDFKNTGSGL-----LGMANIDL-----EKSRGTGDEII 114
DB 153 LLSYAFIVVTILKIPSAEGRHKAFSTCASHLTVVVHYGFASVYILKPKGPKSLEGDTLM 212
QY 115 LPRGLEVTY 123
DB 213 ---GITYTV 218

RESULT 37

US-09-328-352-5429

; Sequence 5429, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 5429

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-5429

Query Match 7.2%; Score 69.5; DB 4; Length 353;
Best Local Similarity 22.0%; Pred. No. 16;
Matches 35; Conservative 28; Mismatches 63; Indels 33; Gaps 6;
QY 40 YCNASVTSVKGNTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLGM 99
DB 3 YC-----AVKNSKSLMHVLSMSILLSL-----SSTSPAEVLNPNSSGSTGT 44
QY 100 ANIDLEKSRGT-----DEILLPRG---LEYTVECTCEDCIKSKPKV-----DSDHCFPL 146
DB 45 ASLNSAADASQLNDEDEDEPTQGSTSVTTILRGSNAPRVITSAPKVPAPIRDTVGYNQA 104
QY 147 PAMEEGATILVTTKTD--YCKSLPAALSATEIEKISISA 183
DB 105 PSVSARAALVMDAQOTGEVLYSKNTNASVPISATIKLMTA 143

RESULT 38

US-09-695-481-2

; Sequence 2, Application US/09695481

; Patent No. 6534287

; GENERAL INFORMATION:

; APPLICANT: STORMANN, THOMAS M.

; APPLICANT: LEVINTHAL, CYNTHIA

; APPLICANT: STORJOHANN, LAURA

; APPLICANT: HAMMERLAND, LANCE G.

; APPLICANT: KRAPCHO, KAREN J.

; APPLICANT: NPS PHARMACEUTICALS, INC.

; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR

; FILE REFERENCE: 1094.2.6

; CURRENT APPLICATION NUMBER: US/09/695,481

; PRIOR APPLICATION NUMBER: 2000-10-24

; PRIOR FILING DATE: 60/161,481

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 942

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-695-481-2

Query Match 7.2%; Score 69.5; DB 4; Length 942;
Best Local Similarity 24.8%; Pred. No. 65;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;
QY 8 CSONEY-FDSLHACIPCOLRCSNTPPLTCQRYCNASVTSVKGNTN-----AILWTCLG 61
DB 537 CXENEIVFDE--YTCACQLG-SWPTDDLIT---GCDLIPVOYLRWGDPPEPIAAVVFACLG 590
QY 62 LSLIISLAVFVLMFLLR-----KISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEILLP 116
DB 591 --LLATLFTVTVFIIYRDTFVVKSSSREL-----YIIL 622
QY 117 RGLTYTVEEC---TCEDCIKSKPKVSDHCF-----PLPAMEEGATILVTTKTN---- 162
DB 623 AGI-----CLGYLCTFCLIAKPK--QIYCLQRIIGIGLSPAMYSALV---TKTNRIAR 671

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/660,148
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-148-5

Query Match 7.2%; Score 69.5; DB 3; Length 1212;
Best Local Similarity 24.6%; Pred. No. 94;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSQNEY-FDSLHACIPCOLRCSNTPLTCQRYCNASVTSVKGTV-----AILWTCLG 61
DB 537 CKENEYVFDE--YTKACQLG-SWPTDLDLT---GCDLIPVQYLRWGDPEPIAAVVFACLG 590
QY 62 LSLIISLAVFLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEILP 116
DB 591 --LLATLFVTVFIIYRDTVPVKSSSREL------YIIL 622
QY 117 RGLTYVEEC---TCEDCIKSKPKVDSHCF-----PLPAMEEGATILVTTKTN--- 162
DB 623 AGI-----CLGYLCTFCLIAKPK--QIYCYLQRIIGLSPAMYSALV---TKTNRIAR 671
QY 163 -----DYCKSLPAALSA 174
DB 672 ILAGSKKIKCTKPRFMSA 690

RESULT 42
US-09-695-481-7
; Sequence 7, Application US/09695481
; Patent No. 6534287
; GENERAL INFORMATION:
; APPLICANT: STORMANN, THOMAS M.
; APPLICANT: LEVINTHAL, CYNTHIA
; APPLICANT: STORJOHANN, LAURA
; APPLICANT: HAMMERLAND, LANCE G.
; APPLICANT: KRAPCHO, KAREN J.
; APPLICANT: NPS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; FILE REFERENCE: 1094.2.6
; CURRENT APPLICATION NUMBER: US/09/695,481
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/161,481
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1212
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-695-481-7

Query Match 7.2%; Score 69.5; DB 4; Length 1212;
Best Local Similarity 24.6%; Pred. No. 94;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSQNEY-FDSLHACIPCOLRCSNTPLTCQRYCNASVTSVKGTV-----AILWTCLG 61
DB 537 CKENEYVFDE--YTKACQLG-SWPTDLDLT---GCDLIPVQYLRWGDPEPIAAVVFACLG 590
QY 62 LSLIISLAVFLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLEKSRGTDEILP 116
DB 591 --LLATLFVTVFIIYRDTVPVKSSSREL------YIIL 622
QY 117 RGLTYVEEC---TCEDCIKSKPKVDSHCF-----PLPAMEEGATILVTTKTN--- 162
DB 623 AGI-----CLGYLCTFCLIAKPK--QIYCYLQRIIGLSPAMYSALV---TKTNRIAR 671
QY 163 -----DYCKSLPAALSA 174
DB 672 ILAGSKKIKCTKPRFMSA 690

RESULT 43
US-08-459-568-2
; Sequence 2, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-568-2

Query Match 7.2%; Score 69.5; DB 2; Length 1706;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

QY 34 PLTCQRYCNASVTSVKGTVNAILWTCLGLSLIISLAVFLMFLLRKISSPLKDEFKNTG 93
DB 598 PVTVE-----ITQNIKSTQV-----SVTDDLKDSPTSST- 626
QY 94 SGLLGMANIDLEKSRGTDEIILPRGLETVVEECTCEDCIKSKP-----KVDSHCHPPLP 147
DB 627 -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLPLSLISITABVWSFH----- 674
QY 148 AMEEGATILVTTKNDYCK-----SLPAALSATEIEK 179
DB 675 -KSKG--VYLSSKLQQLQTDKLTUPAGFSAAEIPK 708
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-586-472-2

Query Match 7.2%; Score 69.5; DB 3; Length 1706;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

Qy 34 PLTCQRYCNASVTVNSVGTNAILWTCIGLSLIISLAVFLMLRLKISSPLKDEPKNTG 93
Db 598 PVTVE-----ITONIKSTQV-----SVTDDLKXSPSST- 626

Qy 94 SGLLGWANIIDLEKSRGTDEIILPRGLETVVECTCEDCIKSKP-----KVDSHCHCPPLP 147
Db 627 -----NCESKKRRRTASPPVLPKIKTETESDSTAPSCSLPLSISTAEVVSFH----- 674

Qy 148 AMEGATILVTTKNDYCK-----SLPAALSATEIEK 179
Db 675 -KEKG--VYLSSKQLQQLQDQKLTLPAGPSAAEIPK 708

RESULT 47
US-09-528-706-2
; Sequence 2, Application US/09528706
; Patent No. 646895
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683

; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-528-706-2

Query Match 7.2%; Score 69.5; DB 4; Length 1706;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

Qy 34 PLTCQRYCNASVTVNSVGTNAILWTCIGLSLIISLAVFLMLRLKISSPLKDEPKNTG 93
Db 598 PVTVE-----ITONIKSTQV-----SVTDDLKXSPSST- 626

Qy 94 SGLLGWANIIDLEKSRGTDEIILPRGLETVVECTCEDCIKSKP-----KVDSHCHCPPLP 147
Db 627 -----NCESKKRRRTASPPVLPKIKTETESDSTAPSCSLPLSISTAEVVSFH----- 674

Qy 148 AMEGATILVTTKNDYCK-----SLPAALSATEIEK 179
Db 675 -KEKG--VYLSSKQLQQLQDQKLTLPAGPSAAEIPK 708

RESULT 48
US-09-125-028-2
; Sequence 2, Application US/09125028A
; Patent No. 6190707
; GENERAL INFORMATION:
; APPLICANT: WADOUX, Isabelle
; APPLICANT: COLAVIZZA, Didier
; APPLICANT: LOJEZ, Annie
; TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS
; FILE REFERENCE: levure sensible froid
; CURRENT APPLICATION NUMBER: US/09/125,028A
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: PCT/FR97/00254
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2496
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-125-028-2

Query Match 7.2%; Score 69.5; DB 3; Length 2496;
Best Local Similarity 24.8%; Pred. No. 2.6e+02;
Matches 34; Conservative 17; Mismatches 49; Indels 37; Gaps 5;

Qy 66 ISLAVFLMFLRLKISSPLKDE-----FKYTGSLGLGHANIDL----- 104
Db 1219 ILLDVDPFLFFAKSLLEQLYSENVMQVLDDEIGIVKRLSNLQEGITSINIDIHAYL 1278
Qy 105 -----EKSRTGDEIILPRGLETVVECTCEDCIKSKPKVDSHCHCPPLPAMEEGATILVTT 159
Db 1279 NLIWQETGEGFELYLDR-IDYQMS-----KSLKQRTNKLLLEVALAKVTVRTV 1330
Qy 160 ---KTNDYCKSLPAALS 173
Db 1331 NQKNPDLSEDRPPALS 1347

RESULT 49
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US-08-894-344C-2
; Sequence 2, Application US/08894344C
; Patent No. 6172196
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, Hideki
; APPLICANT: TOKAI, Masaya
; APPLICANT: KIKUCHI, Yasuhiro
; APPLICANT: OUCHI, Koza
; TITLE OF INVENTION: DNA ENCODING PROTEIN COMPLEMENTING
; TITLE OF INVENTION: YEAST
; TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELIA, HARPER & SCINTO
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1440 Kb storage.
; COMPUTER: IBM PS/V
; OPERATING SYSTEM: MS-DOS Ver3.30
; SOFTWARE: PATENT AID Ver1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894.344C
; FILING DATE: 15-AUGUST-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP343700/95
; FILING DATE: 28-DECEMBER-1995
; APPLICATION NUMBER: PCT/JP96/03862
; FILING DATE: 27-DECEMBER-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-218-2100
; TELEFAX: 212-218-2200
; INFORMATION FOR SEQ ID NO: 2 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2958 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; STRAIN: X2180-1B
; US-08-894-344C-2

Query Match 7.2%; Score 69.5; DB 3; Length 2958;
Best Local Similarity 24.8%; Pred. No. 3.4e+02;
Matches 34; Conservative 17; Mismatches 49; Indels 37; Gaps 5;
QY 66 ISLAVFVLMFLRLKISSPLKDE-----FKWTGSLGGMANIDL----- 104
Db 1219 ILLDVPDLFFFAKSLLEQLYSENVMVQLDDIEIGIVKRLSNLQEGITSINIDIHAYL 1278
QY 105 -----EKSRGTDEIILPRGLYTVBECTCECIKSKPKVDSHDHCFPLPAMEEGATILVTT 159
Db 1279 NLIWQETGEGFELYLDR-IDYQSE-----KSLEKRNKLLVAAAKVKTVRTV 1330
QY 160 ---KTNDYCKSLPAALS 173
Db 1331 NQKNPDLSEDRPPALS 1347

RESULT 50
US-08-579-940-7
; Sequence 7, Application US/08579940
; Patent No. 5977315
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Kohler, Heinz

; APPLICANT: Poon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; TITLE OF INVENTION: 3H1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,940
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 30414-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-940-7
Query Match 7.2%; Score 69; DB 2; Length 324;
Best Local Similarity 36.0%; Pred. No. 16;
Matches 18; Conservative 9; Mismatches 15; Indels 8; Gaps 2;
QY 111 DEILPRGLYTVBECTCECIKSKPKVDSHDHCFPLPAMEEGATILVTTK 160
Db 94 DKKIVPR-----DCGCKPCICTVPEVSSVFIFP-PKPKDVLITLTPK 135
Search completed: January 28, 2005, 19:48:39
Job time : 50.9541 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:37:53 ; Search time 36.3395 Seconds
(without alignments)
335.635 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201
Sequence: 1 CSONEYFDSLLHACIPQLRCSSNTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 201 | 100.0 | 34 | 5 | Aae15486 Human B-C |
| 2 | 201 | 100.0 | 34 | 6 | Ada49366 Human BCM |
| 3 | 201 | 100.0 | 51 | 5 | Aae15485 Human B-C |
| 4 | 201 | 100.0 | 58 | 5 | Aae15501 Human B-C |
| 5 | 201 | 100.0 | 181 | 5 | Aae15484 Human B-C |
| 6 | 201 | 100.0 | 184 | 3 | Aab08843 Amino aci |
| 7 | 201 | 100.0 | 184 | 3 | Aay94001 A human B |
| 8 | 201 | 100.0 | 184 | 4 | Aae09241 Human BCM |
| 9 | 201 | 100.0 | 184 | 4 | Aay71979 Human B-C |
| 10 | 201 | 100.0 | 184 | 4 | Aab60698 Human BAF |
| 11 | 201 | 100.0 | 184 | 4 | Aae00506 Human B C |
| 12 | 201 | 100.0 | 184 | 5 | Abb81487 Human BCM |
| 13 | 201 | 100.0 | 184 | 5 | Abp54694 Metastati |
| 14 | 201 | 100.0 | 184 | 5 | Aae28961 Human B-C |
| 15 | 201 | 100.0 | 184 | 6 | Aae35216 Human B-C |
| 16 | 201 | 100.0 | 184 | 6 | Ada49361 Human BCM |
| 17 | 201 | 100.0 | 184 | 6 | Abp40082 Human Gen |
| 18 | 201 | 100.0 | 184 | 6 | Abp60552 Human tum |
| 19 | 201 | 100.0 | 184 | 6 | Abp97717 Amino aci |
| 20 | 201 | 100.0 | 184 | 7 | Adp67527 Human Lyl |
| 21 | 201 | 100.0 | 184 | 7 | Adg43715 Human B-C |
| 22 | 201 | 100.0 | 184 | 8 | Adk00756 Native hu |
| 23 | 201 | 100.0 | 283 | 5 | Aae15488 Human BCM |
| 24 | 201 | 100.0 | 288 | 5 | Abg95060 Human tra |
| 25 | 201 | 100.0 | 302 | 4 | Aab60699 Mouse Irg |

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| 26 | 201 | 100.0 | 302 | 4 | Aae00507 Human BCM |
| 27 | 201 | 100.0 | 302 | 7 | Adg43717 Human B-C |
| 28 | 159.5 | 79.4 | 157 | 4 | Aab60700 Human BAF |
| 29 | 151 | 75.1 | 26 | 3 | Adi53060 Human BCM |
| 30 | 136 | 67.7 | 185 | 3 | Aab08844 Amino aci |
| 31 | 136 | 67.7 | 185 | 4 | Aay71980 Murine B |
| 32 | 136 | 67.7 | 185 | 5 | Aae15490 Mouse B C |
| 33 | 136 | 67.7 | 281 | 5 | Aae15489 Mouse BCM |
| 34 | 124 | 61.7 | 42 | 6 | Abj38417 TALL-1 re |
| 35 | 93.5 | 46.5 | 117 | 5 | Aae15491 Human-mur |
| 36 | 90.5 | 45.0 | 24 | 3 | Aae15492 Human-mur |
| 37 | 71.5 | 35.6 | 249 | 3 | Aay94006 A murine |
| 38 | 67.5 | 33.6 | 1548 | 7 | Adc71568 Mouse sub |
| 39 | 67.5 | 33.6 | 1877 | 7 | Abb80243 Murine su |
| 40 | 66.5 | 33.1 | 33 | 5 | Aae15495 Human TAC |
| 41 | 66.5 | 33.1 | 33 | 6 | Ada49368 Human TAC |
| 42 | 66.5 | 33.1 | 37 | 5 | Aau10951 Human AGP |
| 43 | 66.5 | 33.1 | 59 | 5 | Aae15500 Human TAC |
| 44 | 66.5 | 33.1 | 166 | 2 | Aaw75785 Human TAC |
| 45 | 66.5 | 33.1 | 166 | 5 | Aae15494 Human TAC |
| 46 | 66.5 | 33.1 | 171 | 8 | Adn03188 Human TAC |
| 47 | 66.5 | 33.1 | 265 | 4 | Aae09244 Human TAC |
| 48 | 66.5 | 33.1 | 266 | 6 | Abp97723 Amino aci |
| 49 | 66.5 | 33.1 | 291 | 5 | Aau10949 Human AGP |
| 50 | 66.5 | 33.1 | 293 | 2 | Aaw75783 Human lym |
| 51 | 66.5 | 33.1 | 293 | 3 | Aay36312 Human neu |
| 52 | 66.5 | 33.1 | 293 | 3 | Aay94000 A transme |
| 53 | 66.5 | 33.1 | 293 | 4 | Aae09240 Human TAC |
| 54 | 66.5 | 33.1 | 293 | 4 | Aay71914 Human tum |
| 55 | 66.5 | 33.1 | 293 | 5 | Aao14130 Human tra |
| 56 | 66.5 | 33.1 | 293 | 5 | Abb81488 Human TAC |
| 57 | 66.5 | 33.1 | 293 | 5 | Aau99512 Human TAC |
| 58 | 66.5 | 33.1 | 293 | 5 | Aae28962 Human TAC |
| 59 | 66.5 | 33.1 | 293 | 5 | Aau75408 Tumour ne |
| 60 | 66.5 | 33.1 | 293 | 5 | Aau09900 Human AGP |
| 61 | 66.5 | 33.1 | 293 | 5 | Aae15493 Human tra |
| 62 | 66.5 | 33.1 | 293 | 5 | Abg71496 Human tum |
| 63 | 66.5 | 33.1 | 293 | 6 | Aae35211 Human TAC |
| 64 | 66.5 | 33.1 | 293 | 6 | Abp60551 Human tum |
| 65 | 66.5 | 33.1 | 293 | 6 | Abp97716 Amino aci |
| 66 | 66.5 | 33.1 | 293 | 6 | Aao29592 Human DIT |
| 67 | 66.5 | 33.1 | 293 | 7 | Adf72628 Human tum |
| 68 | 66.5 | 33.1 | 293 | 7 | Adf77379 Human tum |
| 69 | 66.5 | 33.1 | 293 | 8 | Adk00754 Native hu |
| 70 | 66.5 | 33.1 | 293 | 8 | Adj92514 Human TAC |
| 71 | 66.5 | 33.1 | 293 | 8 | Adn03174 Human TAC |
| 72 | 66.5 | 33.1 | 294 | 8 | Adk00765 hTACi spl |
| 73 | 66.5 | 33.1 | 312 | 5 | Aao14135 Protein o |
| 74 | 66.5 | 33.1 | 332 | 6 | Aae35228 Human TAC |
| 75 | 66.5 | 33.1 | 334 | 6 | Aao14133 Protein o |
| 76 | 66.5 | 33.1 | 344 | 6 | Aae35224 Human TAC |
| 77 | 66.5 | 33.1 | 348 | 6 | Aae35225 Human TAC |
| 78 | 66.5 | 33.1 | 357 | 6 | Aae35226 Human TAC |
| 79 | 66.5 | 33.1 | 366 | 5 | Aao14132 Protein o |
| 80 | 66.5 | 33.1 | 392 | 6 | Aae35223 Human TAC |
| 81 | 66.5 | 33.1 | 397 | 5 | Aae15498 Human TAC |
| 82 | 66.5 | 33.1 | 404 | 5 | Aao14136 Protein o |
| 83 | 61 | 30.3 | 1887 | 6 | Abu12113 Human pro |
| 84 | 61 | 30.3 | 1887 | 6 | Abb80242 Human sub |
| 85 | 61 | 30.3 | 1887 | 7 | Adm29324 Human nov |
| 86 | 59.5 | 29.6 | 138 | 5 | Abp69063 Human pol |
| 87 | 59.5 | 29.6 | 353 | 4 | Abb71555 Drosophil |
| 88 | 59.5 | 29.6 | 418 | 5 | Abb08238 Human 567 |
| 89 | 59.5 | 29.6 | 581 | 7 | Adb64650 Human pro |
| 90 | 59.5 | 29.6 | 735 | 5 | Aag68258 Human POL |
| 91 | 59.5 | 29.6 | 735 | 6 | Abu12091 Novel hum |
| 92 | 59.5 | 29.6 | 845 | 5 | Aag68259 Human POL |
| 93 | 59.5 | 29.6 | 845 | 6 | Abu12092 Novel hum |
| 94 | 59.5 | 29.6 | 845 | 7 | Aae38807 Human POL |
| 95 | 59.5 | 29.6 | 880 | 7 | Adb64680 Human pro |
| 96 | 59.5 | 29.6 | 897 | 4 | Aag65887 Amino aci |
| 97 | 59.5 | 29.6 | 897 | 4 | Abg06309 Novel hum |
| 98 | 59.5 | 29.6 | 897 | 5 | Abg91402 Primate L |

99 59.5 29.6 897 7 ADE07852 Novel pro
100 59.5 29.6 897 7 ADE08940 Novel pro

ALIGNMENTS

RESULT 1
AAE15486
ID AAE15486 standard; peptide; 34 AA.

XX AAE15486;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

OS WO200187979-A2.

PN 22-NOV-2001.

PD 14-MAY-2001; 2001WO-US015567.

PF 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.

XX Claim 1; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TAC1 (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein cysteine-rich consensus region

XX Sequence 34 AA;

XX

Query Match 100.0%; Score 201; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSNTPTPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSNTPTPLTCQRYC 34

RESULT 2

ADA49366

ID ADA49366 standard; peptide; 34 AA.

XX ADA49366;

DT 20-NOV-2003 (first entry)

DE Human BCMA cysteine rich domain.

XX TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
KW antiarthritic; dermatological; antidiabetic; neuroprotective;
KW antichyroid; antipyretic; nephrotropic; vasotropic; vaccine;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW insulin dependent diabetes mellitus; multiple sclerosis;
KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
KW pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
KW cysteine rich domain.

OS Homo sapiens.

PN WO2003035846-A2.

PD 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348962P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.

XX Disclosure; Page 616; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting bkg; strands
CC D and E that reduces the biological activity of the TALL-1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, antirheumatic, antiinflammatory, antichyroid,
CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. It is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarteritis nodosa. The present sequence represents a cysteine rich
CC domain (CRD) module of human BCMA.

CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein extracellular domain
XX
SQ Sequence 51 AA; Query Match 100.0%; Score 201; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.5e-18; Mismatches 0; Indels 0; Gaps 0;
Matches 34; Conservative 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 34
| | | | | | | | | | | | | | | | | | | |
Db 5 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYC 38

RESULT 4
AAE1501
ID AAE15501 standard; peptide; 58 AA.
XX
AC AAE15501;
XX
DT 12-MAR-2002 (first entry)
XX
Human B cell maturation protein cysteine rich extracellular region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX Homo sapiens.
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
PA
PI Theill LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.

XX Disclosure; Fig 13; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70), a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple

CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease, or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34

DB 8 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 41

RESULT 7

AA94001

ID AA94001 standard; protein; 184 AA.

AC AA94001;

DT 20-OCT-2000 (first entry)

DE A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

OS Homo sapiens.

PN WO200040716-A2.

PD 13-JUL-2000.

PF 07-JAN-2000; 2000WO-US000396.

PR 07-JAN-1999; 99US-00226533.

PA (ZYMO) ZYMOGENETICS INC.

PI Gross JA, Xu W, Madden K, Yee DP;

DR WPI; 2000-452538/39.

DR N-PSDB; AAA58559.

XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Disclosure; Page 152; 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting znf4 activity. Znf4 is a TNF ligand. They may also be used

CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 34

DB 8 CSQNEYFDSLHACIPQLRCSSTPPLTCQRYC 41

RESULT 8

AAE09241

ID AAE09241 standard; protein; 184 AA.

AC AAE09241;

DT 19-NOV-2001 (first entry)

DE Human BCMA protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

OS Homo sapiens.

PN WO200160397-A1.

PD 23-AUG-2001.

PF 28-NOV-2000; 2000WO-US032378.

PR 16-FEB-2000; 2000US-0182938P.

PR 22-AUG-2000; 2000US-0226986P.

PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;

DR WPI; 2001-541628/60.

DR N-PSDB; AAD15902.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.

XX Example 2; Fig 2; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction

CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human BCMA protein
 XX
 XX Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYC 34
 DB 8 CSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYC 41
 RESULT 9
 ID AAY71979 standard; protein; 184 AA.
 AC AAY71979;
 XX
 XX 28-MAR-2001 (first entry)
 DT Human B cell maturation factor (BCMA) protein.
 DE
 DE Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Domain 1..62
 FT /label= Extracellular_domain
 XX
 XX WO200068378-A1.
 XX
 XX 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US012266.
 XX
 XX 06-MAY-1999; 99US-0132892P.
 XX
 XX 01-MAY-2000; 2000US-0201012P.
 XX
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 XX Shu HS;
 XX
 XX WPI; 2001-016094/02.
 XX
 XX N-PSDB; AAD02125.
 XX
 XX Isolated TALL-1 protein is used to identify compounds that regulate B
 XX lymphocyte proliferation, used to treat B lymphocyte associated
 XX autoimmune disorders.
 XX
 XX Claim 37; Page 104-105; 112pp; English.
 XX
 XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
 XX related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
 XX proteins (including homologues), and their antibodies. The invention in
 XX particular relates to methods for regulating the interaction between TALL
 XX -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 XX regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 XX TALL-1 protein is useful for identifying compounds that regulate B
 XX lymphocyte proliferation. It is also useful for treating B lymphocyte
 XX associated autoimmune disorders like rheumatoid arthritis, systemic lupus

CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA) protein.
 CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
 CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
 CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
 CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
 CC increases with B lymphocyte maturation
 XX
 XX Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYC 34
 DB 8 CSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYC 41
 RESULT 10
 ID AAB60698 standard; protein; 184 AA.
 AC AAB60698;
 XX
 XX 22-MAY-2001 (first entry)
 DT Human BAFF receptor (BAFF-R).
 DE
 DE Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 XX WO200112812-A2.
 XX
 XX 22-FEB-2001.
 XX
 XX 16-AUG-2000; 2000WO-US022507.
 XX
 XX 17-AUG-1999; 99US-0149378P.
 XX
 XX 11-FEB-2000; 2000US-0181684P.
 XX
 XX 18-FEB-2000; 2000US-0183536P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 XX
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 XX Thompson J;
 XX
 XX WPI; 2001-202866/20.
 XX
 XX N-PSDB; AAF59998.
 XX
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 XX lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 XX chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 XX
 XX Claim 20; Fig 1; 59pp; English.
 XX
 XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
 XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the

CC treatment of a variety of immune-related disorders. BAFF-R is a member of
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAFF-R
CC proteins or BAFF-R specific antibodies may be used for treating,
CC suppressing or altering an immune response involving a signalling pathway
CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents human BAFF-R
XX
SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 34
Db 8 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 11
AAE00506
ID AAE00506 standard; protein; 184 AA.

XX AC AAE00506;
XX DT 31-JUL-2001 (first entry)
XX DE Human B cell maturation protein (BCMA).
XX KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF;
KW tumour necrosis factor; BCMA; B cell maturation protein.
XX OS Homo sapiens.
XX PN WC200124811-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US027579.
XX PR 06-OCT-1999; 99US-0157933P.
XX PR 11-FEB-2000; 2000US-0181807P.
XX PR 30-JUN-2000; 2000US-0215688P.
XX PA (BIOJ) BIOGEN INC.
XX PA (APOT-) APOTECH R & D SA.
XX PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX WPI; 2001-266242/27.
XX DR N-PSDB; AAD03844.
XX

PT Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)

PT antagonist.

XX Claim 3; Fig 3A; 85pp; English.

XX CC The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or carcinoma.
XX The method involves administering a composition comprising A
XX Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
XX maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX diseases, renal disorders, B-cell lympho-proliferative disorders,
XX immunosuppressive diseases, organ transplantation, inflammation and human
XX immunodeficiency virus (HIV), and for treating, suppressing or altering
XX an immune response involving a signalling pathway between APRIL-R and its
XX ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
XX is human APRIL-R also referred as BCMA or BCM protein

SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 34
Db 8 CSQNEVFDSLHACIPQLRCSNTPLTCQRYC 41

RESULT 12

ABB81487
ID ABB81487 standard; protein; 184 AA.

XX AC ABB81487;
XX DT 02-SEP-2002 (first entry)
XX DE Human BCMA receptor related protein SEQ ID NO:7.

XX KW Human; Tnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.

XX OS Homo sapiens.

XX PN WO200238766-A2.

XX PD 16-MAY-2002.

XX PF 05-NOV-2001; 2001WO-US047018.

XX PR 07-NOV-2000; 2000US-0246449P.

XX PR 20-DEC-2000; 2000US-0257131P.

XX PR 28-JUN-2001; 2001US-0301715P.

XX PR 29-AUG-2001; 2001US-0315565P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Henne RM, Grant FJ;
XX WPI; 2002-508212/54.
XX DR

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
 PT renal failure or renal disease and lymphoma.
 XX
 PS Disclosure; Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 13

ABP54694
 ID ABP54694 standard; protein; 184 AA.

XX AC ABP54694;

XX 30-DEC-2002 (first entry)

XX Metastatic colorectal cancer-associated polypeptide.

XX Colorectal cancer; metastasis; differential expression; cytostatic;
 KW diagnosis; gene therapy; vaccine.

XX Homo sapiens.

XX WO200268677-A2.

XX 06-SEP-2002.

XX 27-FEB-2002; 2002WO-US006001.

XX 27-FEB-2001; 2001US-027206P.

XX 02-APR-2001; 2001US-0281149P.

XX 17-APR-2001; 2001US-0284555P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Mack DH, Markowitz SD;

XX WPI; 2002-698677/75.

XX N-PSDB; ABQ81560.

XX New genes that are up- or down-regulated in colorectal cancer, useful for
 PT diagnosing colorectal cancer in a subject, or for identifying modulators
 PT of colorectal cancer-associated proteins and genes for treating
 PT colorectal cancer.

XX Claim 8; Page 255; 260pp; English.

XX The present sequence is the protein sequence of a human polypeptide
 CC encoded by a gene that exhibits decreased expression in colon cancer-
 CC derived metastases compared to normal colon tissue. It is an example of
 CC claimed polypeptides that are encoded by genes which are differentially
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are
 CC useful in diagnostic and prognostic assays, for raising antibodies useful
 CC e.g. in immunotherapy, and in screening for modulator compounds of
 CC therapeutic value

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 14

AAE28961
 ID AAE28961 standard; protein; 184 AA.

XX AC AAE28961;

XX 27-JAN-2003 (first entry)

XX Human B-cell maturation antigen (BCMA).

XX Human; tumour; B-cell maturation antigen; transmembrane activator;
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; Gene therapy;
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 KW BCMA; multiple myeloma.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..54 "Antigenic epitope"

XX Domain 1..48 "note= "Extracellular domain"

XX Region 8..41 "note= "Cysteine rich region"

XX WO200265516-A2.

XX 29-AUG-2002.

XX 06-FEB-2002; 2002WO-US003500.

XX 20-FEB-2001; 2001US-0270274P.

XX 12-APR-2001; 2001US-0283447P.

XX (ZYMO) ZYMOGENETICS INC.

XX Kindvogel W;

XX WPI; 2002-723183/78.

XX N-PSDB; AAD46410.

XX B-cell maturation antigen and transmembrane activator and calcium-
 PT modulator and cyclophilin ligand-interactor, useful for treating
 PT disorders e.g. inflammation or lymphoma.

XX Disclosure; Page 63; 67pp; English.

XX The invention relates to the manufacture of a composition for inhibiting

CC the proliferation of tumour cells. The method involves using an antibody

CC component that binds both the B-cell maturation antigen (BCMA) and the

CC transmembrane activator and calcium-modulator and cyclophilin ligand-

CC interactor (TACI). BCMA and TACI binding antibody compositions are useful

CC for inhibiting proliferation of tumour cells, particularly inhibiting

CC ZTNF4 activity in a mammal associated with increased endogenous antibody

CC production or a disorder consisting of neoplasm, chronic lymphocytic

CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation

CC lymphoproliferative disease or light chain gammopathy or inflammation

CC e.g. asthma. The invention is also useful in gene therapy. The present is

CC human BCMA protein

XX

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDSLHACIPQLRCSNTPTPLTCQRYC 34

DB 8 CSQNEVFDSLHACIPQLRCSNTPTPLTCQRYC 41

RESULT 15

AAE35216

ID AAE35216 standard; protein; 184 AA.

XX

AC AAE35216;

XX

DT 28-MAY-2003 (first entry)

XX

DE Human B-cell maturation receptor (BCMA) protein.

XX

KW Transmembrane activator; calcium modulator; nephrotropic; antibacterial;

KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;

KW anaemia; gene therapy; cystostatic; antiinflammatory; immunosuppressive;

KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;

KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;

KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;

KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;

KW B-cell maturation receptor; BCMA; receptor.

XX

OS Homo sapiens.

XX

PN WO200294852-A2.

XX

PD 28-NOV-2002.

XX

PF 20-MAY-2002; 2002WO-US015910.

XX

XX 24-MAY-2001; 2001US-0293343P.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Rixon MW, Gross JA;

XX

XX WPI; 2003-148455/14.

DR N-PSDB; AAD53754.

XX

PT Transmembrane activator and calcium modulator and cyclophilin ligand-

PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or

PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

XX

PS Disclosure; Col 100; 71pp; English.

XX

CC The invention relates to fusion proteins comprising transmembrane

CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)

CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or

CC ZTNF4; and an immunoglobulin group comprising a constant region of an

CC immunoglobulin. The invention is used to manufacture a medicament for

CC inhibiting the proliferation of tumour cells in a mammalian subject. The

CC composition comprising the fusion protein may also be used in treating

CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple

CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal

CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft

CC rejection, anaemia and septic shock. The fusion proteins are also used in

CC gene therapy. The present sequence is human B-cell maturation receptor

CC (BCMA) protein used in the invention

XX

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDSLHACIPQLRCSNTPTPLTCQRYC 34

DB 8 CSQNEVFDSLHACIPQLRCSNTPTPLTCQRYC 41

RESULT 16

ADA49361

ID ADA49361 standard; protein; 184 AA.

XX

AC ADA49361;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human BCMA protein.

XX

KW human; TALL-1; antagonist; immunosuppressive; antirheumatic;

KW antiinflammatory; antiarthritic; dermatological; antidiabetic;

KW neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;

KW vaccine; autoimmune disease; rheumatoid arthritis;

KW systemic lupus erythematosus; insulin dependent diabetes mellitus;

KW multiple sclerosis; myasthenia gravis; Grave's disease;

KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;

KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.

XX

OS Homo sapiens.

XX

PN WO2003035846-A2.

XX

PD 01-MAY-2003.

XX

PF 24-OCT-2002; 2002WO-US034376.

XX

PR 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348962P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX

PA (NAJB-) NAT JEWISH MEDICAL & RES CENT.

XX

PI Zhang G, Shu H, Liu Y, Xu L;

XX

XX WPI; 2003-403345/38.

DR N-PSDB; ADA49360.

XX

PT Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological

PT activity in mammal, has a modification in the region connecting beta

PT strands D and E that reduces the biological activity of TALL-1

PT antagonist.

XX

PS Claim 62; Page 613; 618pp; English.

XX

CC The invention relates to a novel TALL-1 antagonist protein, comprising a

CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID

CC NO:2, by at least one modification in the region connecting E&G; strands

CC D and E that reduces the biological activity of the TALL-1 antagonist as

CC compared to wild-type TALL-1. A protein of the invention has

CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyrretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents human BCMA.
 XX
 XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 41

RESULT 17
 ABR40082
 ID ABR40082 standard; protein; 184 AA.
 XX
 XX
 AC ABR40082;

DT 27-JUN-2003 (first entry)

DE Human Genoxit.

KW Human; genoxit; anorectic; antilipaeamic; antiarteriosclerotic; cardiant;
 KW antidiabetic; hypotensive; ophthalmological; neuroprotective; Family;
 KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super
 KW Type III transmembrane protein; insulin resistance; atherosclerosis;
 KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;
 KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1. .54
 FT /label= Extracellular_domain
 FT Misc-difference 3
 FT /label= Gln, Lys
 FT Domain 55. .77
 FT /label= Transmembrane_domain
 FT Domain 78. .184
 FT /label= Intracellular_domain

XX WO2003013582-A1.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-IB003498.

XX 06-AUG-2001; 2001US-0310754P.

XX (GEST) GENSET SA.

XX Lucas J, Dialynas D, Briggs K;

XX WPI; 2003-266160/26.

XX N-PSDB; ACC00340.

XX New use of agonist or antagonist of Genoxit activity for preventing or
 PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
 PT atherosclerosis.

XX PS Disclosure; Page 32; 35pp; English.

XX

CC The present invention relates to the use of an agonist or antagonist of
 CC Genoxit activity for preventing or treating obesity. Genoxit is a member
 CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
 CC transmembrane protein. The agonists or antagonists of the invention are
 CC useful for treating or preventing obesity-related diseases or disorders,
 CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
 CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
 CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
 CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
 CC complications, e.g. microangiopathic lesions, ocular lesions,
 CC retinopathy, neuropathy and renal lesions
 XX
 XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 34
 |||||
 Db 8 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 41

RESULT 18
 ABP60552
 ID ABP60552 standard; protein; 184 AA.
 XX
 XX
 AC ABP60552;

DT 28-MAR-2003 (first entry)

DE Human tumour necrosis factor BCMA.

KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;
 KW antiarthritic; cytosatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculosatic; antidiabetic;
 KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.
 XX
 OS Homo sapiens.

XX WO200294192-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-US016106.

XX 24-MAY-2001; 2001US-0293100P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM;

XX WPI; 2003-156740/15.

XX Novel isolated antibody that immunospecifically binds tumor necrosis
 PT factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.

XX Disclosure; Page 222; 225pp; English.

XX The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor Delta (TNF-Delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antiallergic, cytosatic, antianaemic,
 CC antipsoriatic, anti-HIV, antiarteriosclerotic, vasotropic, ophthalmological,
 CC tuberculosatic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or

CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculous, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor BCMA
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 34
 DB 8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 41

RESULT 19
 ABP97717
 ID ABP97717 standard; protein; 184 AA.

AC ABP97717;
 DT 28-MAY-2003 (first entry)

DE Amino acid sequence of human BCMA receptor.

XX Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus; BCMA.

XX Homo sapiens.

OS WO2003014294-A2.

PN 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

PR 30-APR-2002; 2002US-0377171P.

XX (GETH) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

DR N-PSDB; ABZ68871.

XX New nucleic acid encoding a TAC1 or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.

PS Disclosure; Fig 2; 153pp; English.

XX The present sequence represents a human BCMA polypeptide. The
 CC specification also describes TAC1 and BR3 polypeptides. TAC1 and BR3 are
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for
 CC preparing a composition for treating systemic lupus erythematosus

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 34
 DB 8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 41

RESULT 20

ADD67527

ID ADD67527 standard; protein; 184 AA.

XX ADD67527;

XX 15-JAN-2004 (first entry)

XX Human Lyl732P protein SEQ ID NO:4.

XX haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
 KW vaccine; immunotherapy; cancer; multiple myeloma cell;
 KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
 KW human.

XX Homo sapiens.

XX WO2003062401-A2.

XX 31-JUL-2003.

XX 22-JAN-2003; 2003WO-US002353.

XX 22-JAN-2002; 2002US-00057475.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
 PI Carter L, McNeill PD;

XX WPI; 2003-598749/56.

DR N-PSDB; ADD67526.

XX New hematological malignancy-related genes and polypeptides, useful for
 PT screening anti-cancer agents, and generating antibodies or
 PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
 PT lymphocytic leukemia.

XX Claim 9; SEQ ID NO 4; 307pp; English.

XX The present invention describes an isolated polynucleotide (I), which is
 CC overexpressed in haematological malignancies, and which encodes a
 CC polypeptide or an immunogenic fragment of the polypeptide. Also
 CC described: (1) an isolated polypeptide; (2) an expression vector
 CC comprising (I) operably linked to an expression control sequence; (3) a
 CC host cell comprising an expression vector; (4) an isolated antibody that
 CC specifically binds to the polypeptide or its immunogenic fragment; and
 CC (5) immunoconjugates comprising the antibody above, or an antibody that
 CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
 CC by (I). (I) has cytostatic and immunostimulant activities, and can be
 CC used in vaccines and immunotherapy. The immunoconjugates are useful in
 CC the manufacture of a medicament, particularly as active ingredients in a
 CC composition for treating cancer, e.g. multiple myeloma cell, chronic
 CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
 CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
 CC The polynucleotide (I) or polypeptide can be used for screening anti-
 CC cancer agents, and generating antibodies or immunoconjugates for treating
 CC or preventing the above-mentioned diseases. The polynucleotide,
 CC polypeptide or antibody can be used for detecting, diagnosing or
 CC prognosticating the haematological malignancies described above. The
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 7; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 21
 ADG43715
 ID ADG43715 standard; protein; 184 AA.

AC ADG43715;
 DT 26-FEB-2004 (first entry)
 DE Human B-cell maturation antigen SEQ ID NO:1.
 XX human; neurodegenerative immunological disorder; demyelination;
 KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
 KW BCMA; multiple sclerosis; neuroprotective; neurotropic; antiinflammatory;
 KW gene therapy.
 XX Homo sapiens.
 OS WO2003072713-A2.
 PN 04-SEP-2003.
 PD
 XX 21-FEB-2003; 2003WO-US005147.
 PF 21-FEB-2002; 2002US-0358427P.
 PR (BIOJ) BIOGEN INC.
 PA Kalled SL, Reid H;
 PI WPI; 2003-721758/68.
 DR N-PSDB; ADG43716.
 XX Treating a neurodegenerative immunological disorder, e.g. demyelination
 PT or inflammation in a mammal comprises administering a B-cell maturation
 PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.
 PS Claim 8; Page 68-69; 72pp; English.
 XX The invention relates to a novel method for treating a neurodegenerative
 CC immunological disorder, demyelination or Central Nervous System (CNS)
 CC inflammation in a mammal. The method comprises administering B-cell
 CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
 CC (the mammal has or is at risk of developing multiple sclerosis). The
 CC method of the invention has neuroprotective, neurotropic, and
 CC antiinflammatory activity, and may have a use in gene therapy. The
 CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
 CC immunological disorder such as multiple sclerosis, demyelination or CNS
 CC inflammation. The present sequence represents human BCMA.

SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 7; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 22
 ADK00756
 ID ADK00756 standard; protein; 184 AA.
 XX

AC ADK00756;
 XX 06-MAY-2004 (first entry)
 DT Native human BCMA.
 DE
 XX CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
 KW Dermatalogical; Immunosuppressive; Antirheumatic; Antiarthritic;
 KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
 KW Antibacterial; antiparasitic; systemic lupus erythematosus;
 KW diabetes mellitus; AIDS; BCMA.
 XX Homo sapiens.
 OS WO2004011611-A2.
 PN 05-FEB-2004.
 PD
 XX 25-JUL-2003; 2003WO-US023421.
 PF 25-JUL-2002; 2002US-0398530P.
 PR (GETH) GENENTECH INC.
 PA Chuntharapai A, Grewal I, Kim KJ, Yan M;
 XX WPI; 2004-143841/14.
 PI N-PSDB; ADK00755.
 DR
 XX New anti-TACI receptor monoclonal antibody, useful for diagnosing and
 PT treating pathological conditions associated with tumor necrosis factor,
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
 PT psoriasis.
 XX Disclosure; SEQ ID NO 6; 110pp; English.
 PS
 XX The present invention relates to an isolated monoclonal antibody which
 CC binds to a transmembrane activator of and CAML interactor (TACI)
 CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI
 CC polypeptide biological activity in mammalian cells, or for diagnosing and
 CC treating pathological conditions associated with TNF and TNF receptor-
 CC related molecules, e.g. cancer or immune-related disease, such as
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or
 CC infectious diseases including AIDS, hepatitis infection, bacterial
 CC infection, fungal infection, protozoal infection and parasitic infection.
 CC The present sequence represents native human BCMA.

SQ Sequence 184 AA;
 Query Match 100.0%; Score 201; DB 8; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.3e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
 DB 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 23
 AAEL15488
 ID AAEL15488 standard; protein; 283 AA.
 XX
 AC AAEL15488;
 XX
 DT 12-MAR-2002 (first entry)
 XX Human BCMA-immunoglobulin Fc region fusion protein.
 DE
 XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytotostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;

KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; aschma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.
 XX Homo sapiens.
 XX WO200187979-A2.
 XX 22-NOV-2001.
 XX 14-MAY-2001; 2001WO-US015567.
 XX 12-MAY-2000; 2000US-0204039P.
 XX 27-JUN-2000; 2000US-0214591P.
 XX 14-MAY-2001; 2001US-00214591.
 XX (AMGE-) AMGEN INC.
 XX Theill LE, Yu G;
 XX WPI; 2002-066686/09.
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX Disclosure; Fig 10B; 94pp; English.
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein
 XX Sequence 283 AA;
 SQ Query Match 100.0%; Score 201; DB 5; Length 283;
 Best Local Similarity 100.0%; Pred. No. 2e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
 DB 5 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 38
 RESULT 24
 ID ABG95060 standard; protein; 288 AA.
 XX AC ABG95060;
 XX 04-DEC-2002 (first entry)
 XX Human translocation (4; 16)(q26; p13) protein.
 XX Chromosome aberration; oncogenic fusion protein; cancer;
 KW

KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX Homo sapiens.
 XX WO200269900-A2.
 XX 12-SEP-2002.
 XX 01-MAR-2002; 2002WO-US006518.
 XX 01-MAR-2001; 2001US-0272751P.
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 XX Fritz LC, Burrows FJ;
 XX WPI; 2002-698710/75.
 XX N-PSDB; ABS73235.
 XX Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 XX Disclosure; Page 189-190; 389pp; English.
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p33), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents a protein encoded by the DNA sequence of a
 CC chromosome aberration
 XX Sequence 288 AA;
 SQ Query Match 100.0%; Score 201; DB 5; Length 288;
 Best Local Similarity 100.0%; Pred. No. 2e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
 DB 112 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 145
 RESULT 25
 ID AAB60699 standard; protein; 302 AA.
 XX AC AAB60699;
 XX 11-SEP-2003 (revised)
 XX 22-MAY-2001 (first entry)
 XX

DE Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
 XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX WO200112812-A2.
 XX 22-FEB-2001.
 XX 16-AUG-2000; 2000WO-US022507.
 XX 17-AUG-1999; 99US-0149378P.
 XX 11-FEB-2000; 2000US-0181684P.
 XX 18-FEB-2000; 2000US-0183536P.
 XX (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 FI Thompson J;
 FI WPI; 2001-202866/20.
 DR N-PSDB; AAF59999.
 DR Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 XX lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 FT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 FT Example 4; Fig 2; 59pp; English.
 PS The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human
 CC BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX Sequence 302 AA;

Query Match 100.0%; Score 201; DB 4; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2,1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIFCOLRCSSNTPLTCQRYC 34
 Db 31 CSQNEYFDSLHACIFCOLRCSSNTPLTCQRYC 64
 RESULT 26
 AAEE0507
 ID AAE00507 standard; protein; 302 AA.
 XX AC AAE00507;
 XX 11-SEP-2003 (revised)
 DT 31-JUL-2001 (first entry)
 XX Human BCMA-Immunoglobulin G Fc region fusion construct.
 XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
 KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
 KW immunoglobulin G; IgG; Fc region.
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX Key Location/Qualifiers
 FH Protein 1..22
 FT /label= Signal peptide
 FT /note= "Derived from murine Ig kappa sequence"
 FT Protein 23..302
 FT /label= Mature_human_BCMA_IgG_Fc_fusion_protein
 FT Region 23..75
 FT /note= "Derived from human BCMA protein"
 FT Domain 24..302
 FT /label= Cysteine rich domain
 FT /note= "Derived from human BCMA"
 FT Region 76..302
 FT /note= "Derived from human IgG Fc region"
 FT WO200124811-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000WO-US027579.
 XX 06-OCT-1999; 99US-0157933P.
 PR 11-FEB-2000; 2000US-0181807P.
 PR 30-JUN-2000; 2000US-0215688P.
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
 WPI; 2001-266242/27.
 DR N-PSDB; AAD03847.
 XX Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 PT antagonist.
 XX Example 1; Fig 3B; 85pp; English.
 PS The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or carcinoma.
 CC The method involves administering a composition comprising A
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
 CC maturation protein (BCM or BCMA) antagonist that antagonises the

CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and human
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering
 CC an immune response involving a signalling pathway between APRIL-R and its
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
 CC is a fusion construct containing human APRIL-R also referred as BCMA or
 CC BCM protein, FC region of human immunoglobulin G (IgG) and a signal
 CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
 CC standardise OS field)

XX SQ Sequence 302 AA;
 Query Match 100.0%; Score 201; DB 4; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34
 |||||
 DB 31 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 64

RESULT 27
 ADG43717
 ID ADG43717 standard; protein; 302 AA.

XX AC ADG43717;

XX DT 26-FEB-2004 (first entry)

XX DE Human B-cell maturation antigen-Fc SEQ ID NO:3.

XX KW human; neurodegenerative immunological disorder; demyelination;
 KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
 KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
 KW gene therapy; mouse.

XX OS Chimeric.

OS Homo sapiens.

OS Mus sp.

XX FH Key Location/Qualifiers

FT Region 1..23 /note= "Murine IgG kappa signal sequence"

FT Region 24..74 /note= "Human BCMA extracellular domain"

FT Region 75..302 /note= "Human Ig heavy chain FC region"

FT FT

FT FT

XX WO2003072713-A2.

PN 04-SEP-2003.

XX PD 21-FEB-2003; 2003WO-US005147.

XX PF 21-FEB-2002; 2002US-0358427P.

XX PR (BIOJ) BIOGEN INC.

XX PA Kalled SL, Reid H;

XX PI WPI; 2003-721758/68.

XX DR N-PSDB; ADG43718.

XX XX

XX PT Treating a neurodegenerative immunological disorder, e.g. demyelination

PT or inflammation in a mammal comprises administering a B-cell maturation

PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.

XX XX

PS Claim 12; Page 70-71; 72pp; English.

XX The invention relates to a novel method for treating a neurodegenerative
 CC immunological disorder, demyelination or Central Nervous System (CNS)
 CC inflammation in a mammal. The method comprises administering B-cell
 CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
 CC (the mammal has or is at risk of developing multiple sclerosis). The
 CC method of the invention has neuroprotective, nontropic, and
 CC antiinflammatory activity, and may have a use in gene therapy. The
 CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
 CC immunological disorder such as multiple sclerosis, demyelination or CNS
 CC inflammation. The present sequence is used in the exemplification of the
 CC invention.

XX SQ Sequence 302 AA;

Query Match 100.0%; Score 201; DB 7; Length 302;
 Best Local Similarity 100.0%; Pred. No. 2.1e-17;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34

|||||

DB 31 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 64

RESULT 28

AAB60700

ID AAB60700 standard; protein; 157 AA.

XX AC AAB60700;

XX DT 22-MAY-2001 (first entry)

XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.

XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

XX immune-related disorder; B-cell growth inhibitor; BCMA;

XX B-cell maturation inhibitor; immunoglobulin production inhibitor;

XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

XX renal disorder; immunosuppressive disorder; HIV infection;

XX organ transplantation; antiinflammatory; systemic lupus erythematosus;

XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;

XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;

XX lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

XX OS Homo sapiens.

XX WO200112812-A2.

XX PD 22-FEB-2001.

XX PF 16-AUG-2000; 2000WO-US022507.

XX PR 17-AUG-1999; 99US-0149378P.

XX PR 11-FEB-2000; 2000US-0181684P.

XX PR 18-FEB-2000; 2000US-0183536P.

XX XX

PA (BIOJ) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;

XX Thompson J;

XX WPI; 2001-202866/20.

XX DR N-PSDB; AAF60000.

XX XX

XX PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell

PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,

PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.

XX XX

XX PS Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known

XX

as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents a human BAFF-R protein sequence as encoded by plasmid PUST535. However, this BAFF-R protein sequence is 27 amino acids shorter than that given in AAB60698

XX Sequence 157 AA;

Query Match 79.4%; Score 159.5; DB 4; Length 157;
Best Local Similarity 90.6%; Pred. No. 2.1e-12;
Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 QNEYPDSLHACIPQCLRCSSNTPLTCQRYC 34

DB 7 QNEYPDSLHACIPQCLRCSSNTPLTCQRYC 35

RESULT 29

ADIS3060
ID ADIS3060 standard; peptide; 26 AA.

XX AC ADIS3060;

XX DT 22-APR-2004 (first entry)

XX DE Human BCMA receptor binding site.

XX KW protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;
XX KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
XX KW antidiabetic; dermatological; antiasthmatic; neutrokin-alpha;
XX KW crystallography; cancer; allergic disorder; autoimmune disease;
XX KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
XX KW systemic lupus erythematosus; asthma; receptor.

XX OS Homo sapiens.

XX EN WO2003050134-A2.

XX PD 19-JUN-2003.

XX PF 07-NOV-2002; 2002WO-US035661.

XX PR 07-NOV-2001; 2001US-0331049P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Oren DE, Arnold E, Volovik Y;

XX WPI; 2003-532895/50.

XX PT New crystalline Neutrokin-alpha protein, useful for designing compounds
XX PT that bind, inhibit or mimic a Neutrokin-alpha protein or enhance the
XX PT activity of a Neutrokin-alpha protein for treating e.g. cancer or
XX PT allergic disorders.

PS Disclosure; Fig 4; 362pp; English.

XX CC The invention relates to a neutrokin-alpha protein in crystalline form.
XX CC The crystalline neutrokin-alpha protein is useful for designing
XX CC molecules that have biological activity or compounds that bind, inhibit
XX CC or mimic a neutrokin-alpha protein and/or enhance the activity of a
XX CC neutrokin-alpha protein. The three-dimensional structure of a neutrokin
XX CC -alpha protein is useful in determining the three-dimensional of other
XX CC neutrokin-alpha proteins and their homologs. The compounds that mimic,
XX CC prevent or inhibit the activity of the protein are useful for treating
XX CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid
XX CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
XX CC erythematosus or asthma. This sequence represents the residues in the
XX CC receptor for binding a cytokine ligand.

SQ Sequence 26 AA;

Query Match 75.1%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYFDSLHACIPQCLRCSSNTPLTC 30

DB 1 EYFDSLHACIPQCLRCSSNTPLTC 26

RESULT 30

AAB08844

ID AAB08844 standard; peptide; 185 AA.

XX AC AAB08844;

XX DT 02-JAN-2001 (first entry)

XX DE Amino acid sequence of murine BCMA polypeptide.

XX KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
XX KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
XX KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX OS Mus musculus.

XX FT Key Location/Qualifiers

XX FT Domain 47..72

XX FT /note= "putative transmembrane domain"

XX PN WO200050633-A1.

XX PD 31-AUG-2000.

XX PF 24-FEB-2000; 2000WO-US004925.

XX PR 24-FEB-1999; 99US-0121485P.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Seed B, Ting A;

XX WPI; 2000-558405/51.

XX PT Identifying a modulator of gene expression for drug designing, by
XX PT contacting a compound library with a cell expressing an anti-cell death
XX PT gene and reporter gene, and determining alteration in reporter gene
XX PT expression.

XX PS Claim 32; Fig 7B; 53pp; English.

XX CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is
XX CC a necrosis factor (NF)-kB activator. The method of the invention is used
XX CC to identify compounds which modulate BCMA activity (and thus NF-kB
XX CC activity). The specification describes a method of identifying a
XX CC polypeptide which increases gene expression from a promoter. The method
XX CC involves contacting a library of with a cell which expresses a

CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the reporter
 CC gene is altered as a result of contact with library. The method is useful
 CC for identifying polypeptides which increase or decrease gene expression
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,
 CC viral infections, inflammatory response, such as rheumatoid arthritis,
 CC inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing
 XX
 SQ Sequence 185 AA;

Query Match 67.7%; Score 136; DB 3; Length 185;
 Best Local Similarity 70.6%; Pred. No. 2.5e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 QY 1 CSONEYFDSLHLHACIPCOLRCSNTPLTCQRYC 34
 | : ||||| ||||| ||||| : |||||
 Db 5 CFHSEYFDSLHLHACKPCHLRCSN--PPATCQPYC 36

RESULT 31
 AAY71980
 ID AAY71980 standard; protein; 185 AA.
 XX AC AAY71980;
 XX AC AAY71980;
 DT 28-MAR-2001 (first entry)
 XX Murine B cell maturation factor (BCMA) protein.
 XX Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-L-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa.
 XX
 OS Mus musculus.
 XX WO200068378-A1.
 XX 16-NOV-2000.
 XX 05-MAY-2000; 2000WO-US012266.
 XX 06-MAY-1999; 99US-0132892P.
 XX 01-MAY-2000; 2000US-0201012P.
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX Shu HS;
 XX WPI; 2001-016094/02.
 XX N-PSDB; AAD02130.
 XX Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders.
 XX
 PS Claim 37; Page 107-108; 112pp; English.
 XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
 CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
 CC proteins (including homologues), and their antibodies. The invention in
 CC particular relates to methods for regulating the interaction between TALL
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
 CC TALL-1 protein is useful for identifying compounds that regulate B
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte

CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.
 CC The present sequence is a murine B cell maturation factor (BCMA). BCMA is
 CC the receptor for TALL-1 protein
 XX
 SQ Sequence 185 AA;

Query Match 67.7%; Score 136; DB 4; Length 185;
 Best Local Similarity 70.6%; Pred. No. 2.5e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 QY 1 CSONEYFDSLHLHACIPCOLRCSNTPLTCQRYC 34
 | : ||||| ||||| ||||| : |||||
 Db 5 CFHSEYFDSLHLHACKPCHLRCSN--PPATCQPYC 36

RESULT 32
 AAE15490
 ID AAE15490 standard; protein; 185 AA.
 XX AC AAE15490;
 XX AC AAE15490;
 DT 12-MAR-2002 (first entry)
 XX Mouse B cell maturation (BCMA) protein.
 XX Mouse; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Mus sp.
 XX WO200187979-A2.
 XX 22-NOV-2001.
 XX 14-MAY-2001; 2001WO-US015567.
 XX 12-MAY-2000; 2000US-0204039P.
 XX 27-JUN-2000; 2000US-0214591P.
 XX 14-MAY-2001; 2001US-00214591.
 XX (AMGB-) AMGEN INC.
 XX Theill LE, Yu G;
 XX WPI; 2002-066686/09.
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumour necrosis factor family
 PT ligand.
 XX
 PS Disclosure; Fig 11; 94pp; English.
 XX The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell

CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein
 CC
 XX Sequence 185 AA;
 SQ

Query Match 67.7%; Score 136; DB 5; Length 185;
 Best Local Similarity 70.6%; Pred. No. 2.5e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPTLCORYC 34
 DB 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 33
 AAEL5489
 ID AAEL5489 standard; protein; 281 AA.
 AC AAEL5489;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse BCMA-human immunoglobulin Fc region fusion protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 OS
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US015567.
 XX
 PR 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.
 PR 14-MAY-2001; 2001US-00214591.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Theill LE, Yu G;
 XX
 XX WPI; 2002-066686/09.
 XX
 DR Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX
 XX Disclosure; Fig 10B; 94pp; English.
 PS
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 281 AA;
 Query Match 67.7%; Score 136; DB 5; Length 281;
 Best Local Similarity 70.6%; Pred. No. 3.8e-09;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPTLCORYC 34
 DB 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 34
 ABJ38417
 ID ABJ38417 standard; protein; 42 AA.
 AC ABJ38417;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE TALL-1 related protein SEQ ID No 197.
 XX
 KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
 KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
 KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
 KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
 KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
 KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200292620-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 13-MAY-2002; 2002WO-US015273.
 XX
 PR 11-MAY-2001; 2001US-0290196P.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Min H, Hsu H;
 XX
 XX WPI; 2003-156719/15.
 XX
 DR New TALL-1-binding polypeptide, useful for modulating the activity of
 PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
 PT autoimmune diseases, cancers or lymphomas.
 XX
 PS Disclosure; Page 26; 236pp; English.
 XX
 CC The invention relates to a novel TALL-1-binding polypeptide comprising a
 CC defined sequence in the specification. The composition is useful in
 CC modulating the activity of TALL-1, and in treating, preventing,
 CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune

CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
 CC lymphoma. The composition may also be used in treating inflammations
 CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
 CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
 CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
 CC and vasculitis. Disorders may be treated with the novel composition using
 CC gene therapy. This sequence represents a TALL-1 related protein of the
 CC invention

CC Sequence 42 AA;

Query Match 61.7%; Score 124; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEFDLSLHACIPQLRC 21
 AAE15491
 |||||
 DB 22 CSQNEFDLSLHACIPQLRC 42

RESULT 35
 AAE15491
 ID AAE15491 standard; protein; 117 AA.

XX AAE15491;

XX
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)

DE Human-murine B cell maturation protein (BCMA) consensus sequence.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.

OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX Disclosure; Fig 11; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/

CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human-murine B cell maturation protein (BCMA) consensus sequence.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 117 AA;

Query Match 46.5%; Score 93.5; DB 5; Length 117;
 Best Local Similarity 69.7%; Pred. No. 0.00042;
 Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

OY 2 SONEYFDSLHACIPQLRCSSNTPPLTCORYC 34
 :|||
 DB 2 AQCEYFDSLHAC-PC-LRCS-----PPTCQ-YC 27

RESULT 36

AAE15492

ID AAE15492 standard; peptide; 24 AA.

XX AAE15492;

XX 29-AUG-2003 (revised)

DT 12-MAR-2002 (first entry)

XX Human-murine BCMA consensus sequence cysteine rich region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.

XX Homo sapiens.

OS Mus sp.

OS Chimeric.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.

XX Disclosure; Fig 11; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human-murine B cell maturation protein (BCMA) consensus sequence
 CC cysteine rich region. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 CC Sequence 24 AA;

Query Match 45.0%; Score 90.5; DB 5; Length 24;
 Best Local Similarity 73.3%; Pred. NO. 0.0002;
 Matches 22; Conservative 0; Mismatches 1; Indels 7; Gaps 4;

Qy 5 EYFDSLHACIPCOLRCSNTPTLCQRYC 34
 |||||
 Db 2 EYFDSLHAC-PC-LRCS-PPTCQ-YC 24

RESULT 37

RAY94006.
 ID AAY94006 standard; protein; 249 AA.

AC AAY94006;

XX 20-OCT-2000 (first entry)

XX A murine znf4, a tumour necrosis factor ligand.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Mus musculus.

XX WO200040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000396.

XX 07-JAN-1999; 99US-00226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX N-PSDB; AAA58566.

XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,

PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 XX
 PS Disclosure; Page 163; 175pp; English.
 XX The present sequence represents murine znf4, a tumour necrosis factor
 CC ligand. The extracellular domains of BR43x2 (an isoform of the
 CC transmembrane activator and CAML-interactor (TACI) receptor), TACI or
 CC BCMA (a related B cell protein) contain a cysteine rich domain, and are
 CC used for inhibiting znf4 activity. They may also be used for inhibiting
 CC BR43x2, TACI or BCMA receptor-ligand engagement associated with activated
 CC or resting B lymphocytes, effector T-cells, or with antibody production.
 CC The antibody production is associated with an autoimmune disease selected
 CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
 CC and rheumatoid arthritis. The znf4 activity and BR43x2, TACI or BCMA
 CC receptor-ligand engagement is associated with asthma, bronchitis,
 CC emphysema, and stage renal failure, glomerulonephritis, vasculitis,
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, graft versus host disease,
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli
 XX
 SQ Sequence 249 AA;

Query Match 35.6%; Score 71.5; DB 3; Length 249;
 Best Local Similarity 35.3%; Pred. NO. 0.57;
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 1 CSONEYFDSLHACIPCOLRCSNTPTLCQRYC 34
 |||||
 Db 6 CPKQYWDSSRKSCVSCALTCQSRS-QRTCTDFC 38

RESULT 38

ADCT71568

ID ADCT71568 standard; protein; 1548 AA.

XX ADCT71568;

XX 18-DEC-2003 (first entry)

DE Mouse subtilisin-like protein convertase 6 (SPC6).

XX neuroleptic; subtilisin-like protein convertase 6 agonist;
 KW subtilisin-like protein convertase 6 antagonist; transgenic;
 KW subtilisin-like protein convertase 6; SPC6; schizophrenia.

XX Mus sp.

XX US2003093824-A1.

XX 15-MAY-2003.

XX 25-JUN-2002; 2002US-00180903.

XX 26-JUN-2001; 2001US-0300978P.

PR 24-SEP-2001; 2001US-0324820P.

XX (ALLE/) ALLEN K D.

XX Allen KD;

XX WPI; 2003-777261/73.

DR N-PSDB; ADCT71567.

XX New transgenic mouse useful in methods for identifying potential
 PT therapeutic agents for treating a variety of diseases, including
 PT schizophrenia, comprises a disruption in a subtilisin-like protein
 PT convertase 6 (SPC6) gene.

XX Disclosure; SEQ ID NO 2; 34pp; English.

XX The invention describes a transgenic mouse (I) comprising a disruption in

CC an subtilisin-like protein convertase (SPC6) gene, where there is no

CC native expression of an endogenous SPC6 gene. The therapeutic agent is

CC administered by inhalation or insufflation or oral, buccal, parenteral,

CC topical, subcutaneous, intraperitoneal, intravenous, intrapleural,

CC intraocular, intraarterial, or rectal route. The transgenic mouse and

CC associated methods are useful for identifying potential therapeutic

CC agents (e.g. SPC6 agonists and antagonists) for treating conditions

CC associated with SPC6. The identified agents are potentially useful for

CC treating diseases such as schizophrenia. The mouse is useful for

CC investigating the biological roles of SPC6. This is the amino acid

CC sequence of mouse SPC6.

XX SQ Sequence 1548 AA;

Query Match 33.6%; Score 67.5; DB 7; Length 1548;

Best Local Similarity 37.8%; Pred. No. 12;

Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPP-----LTCQR 32

Db 1152 CAAVEYWDGSHRCQPCCHKRCSCGSPEDQCYTCPR 1188

RESULT 39

ABB80243

ID ABB80243 standard; protein; 1877 AA.

AC ABB80243;

XX 04-DEC-2003 (first entry)

DT Murine subtilase.

DE

XX Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney;

KW renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;

KW pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;

KW proteinase convertase subtilisin; furin-like repeat; Alzheimer's disease;

KW Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;

KW gastritis; ulcers; urinary incontinence; lupus nephritis;

KW renal transplant rejection; myocardial infarction; erectile dysfunction;

KW ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;

KW congestive heart failure; ischaemia; hypertensive vascular disease.

XX Mus musculus.

XX WO2003060109-A2.

PN 24-JUL-2003.

XX 14-JAN-2003; 2003WO-EP0000253.

XX 15-JAN-2002; 2002US-0347876P.

PR 29-JUL-2002; 2002US-0398734P.

XX (FARB) BAYER AG.

PA Koehler RH;

XX WPI; 2003-608065/57.

DR New subtilase-encoding polynucleotide and its encoded protein, useful for

XX identifying modulators of subtilase activity, and in gene therapy for

PT treating e.g. Alzheimer's disease, cancers, congestive heart failure or

PT ischemia.

PS Disclosure; Page 122-26; 135pp; English.

XX This sequence shows a murine subtilase. The homologous human subtilase

CC coding sequence is located on chromosome 9q21.13. Related EST's are

CC expressed in kidney (renal cell adenocarcinoma), head and neck tissue,

CC heart, multiple sclerosis lesions, cervix, pooled germ cell tumours,

CC uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin

CC protein is a long membrane bound protein which shows 96% identity to

CC human proteinase convertase subtilisin. There are two blocks of 11 furin-

CC like repeats in the C-terminal portion of the protein. It has one

CC transmembrane domain, also in the C-terminal portion, suggesting that the

CC protein is localised on the outside of the membrane. The subtilase

CC polynucleotide and polypeptide are useful for identifying test compounds,

CC which may act as agonists or antagonists at the receptor site and which

CC can be regulated to provide therapeutic effects. Vectors comprising the

CC polynucleotide are useful for modulating the activity of subtilase in a

CC disease, e.g. a central nervous system disorder, a gastrointestinal

CC disorder, cancer, a cardiovascular disorder, a genitourinary disorder, or

CC diabetes. In particular, these diseases are Alzheimer's disease,

CC Parkinson's disease, pain, colon tumour, pre-oesophageal dysphagia,

CC gastritis, ulcers, urinary incontinence, lupus nephritis, renal

CC transplant rejection, pelvic pain, erectile dysfunction, ovary tumour,

CC lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma,

CC congestive heart failure, myocardial infarction, ischaemia, hypertensive

CC vascular diseases, etc. These are also useful for preventing or

CC ameliorating the diseases cited above

XX SQ Sequence 1877 AA;

Query Match 33.6%; Score 67.5; DB 7; Length 1877;

Best Local Similarity 37.8%; Pred. No. 14;

Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPP-----LTCQR 32

Db 1481 CAAVEYWDGSHRCQPCCHKRCSCGSPEDQCYTCPR 1517

RESULT 40

AAE15495

ID AAE15495 standard; peptide; 33 AA.

AC AAE15495;

XX 12-MAR-2002 (first entry)

DT Human TACI cysteine-rich consensus region #1.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;

KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;

KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;

KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;

KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;

KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;

KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;

XX rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

PN 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

PA Theill LE, Yu G;

XX WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane

XX activator and intracellular cyclophilin ligand interactor, by

PT administering a binding partner for APRIL, a tumor necrosis factor family
 XX ligand.

XX Claim 1; Fig 12B; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 PS activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, proctitis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 XX is human TACI cysteine-rich consensus region

SQ Sequence 33 AA;

Query Match 33.1%; Score 66.5; DB 5; Length 33;

Best Local Similarity 32.4%; Pred. No. 0.32;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34

Db 1 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAFC 33

RESULT 41

ADA49368

ID ADA49368 standard; peptide; 33 AA.

AC ADA49368;

XX 20-NOV-2003 (first entry)

XX Human TACI1 cysteine rich domain.

XX TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
 KW antiarthritic; dermatological; antidiabetic; neuroprotective;
 KW antithyroid; antipyretic; nephrotropic; vasotropic; vaccine;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW insulin dependent diabetes mellitus; multiple sclerosis;
 KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
 KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
 KW pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; TACI1; CRD;
 KW cysteine rich domain.

XX Homo sapiens.

XX WO2003035846-A2.

XX 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034376.

XX 24-OCT-2001; 2001US-0345106P.

PR 14-JAN-2002; 2002US-0348922P.

PR 07-FEB-2002; 2002US-0354966P.

PR 13-AUG-2002; 2002US-0403364P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Zhang G, Shu H, Liu Y, Xu L;

XX WPI; 2003-403345/38.

XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
 PT activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.

XX Disclosure; Page 617; 618pp; English.

XX The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting E&G; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antichratic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases: rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents a cysteine rich
 CC domain (CRD) module of human TACI1.

XX Sequence 33 AA;

Query Match 33.1%; Score 66.5; DB 6; Length 33;

Best Local Similarity 32.4%; Pred. No. 0.32;

Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34

Db 1 CPEEQYWDPLLTGTCMSCKTICNHQS-QRTCAFC 33

RESULT 42

AAU10951

ID AAU10951 standard; protein; 37 AA.

AC AAU10951;

XX 12-MAR-2002 (first entry)

XX Human AGP-3 receptor cysteine rich repeat region #1.

XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.

XX Homo sapiens.

XX WO200185782-A2.

XX 15-NOV-2001.

XX 12-FEB-2001; 2001WO-US004568.

XX 11-FEB-2000; 2000US-0181800P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Hsu H;

| | | |
|-----------|--|--|
| XX | 22-APR-2004. | |
| PD | | |
| XX | 10-OCT-2003; 2003WO-US032878. | |
| XX | | |
| XX | 11-OCT-2002; 2002US-0417801P. | |
| PR | | |
| XX | (ZYMO) ZYMOGENETICS INC. | |
| PA | | |
| XX | West JW, Brandt CS, Jaspers SR; | |
| PI | | |
| XX | WPT: 2004-364855/34. | |
| DR | N-PSDB; ADN03187. | |
| DR | | |
| XX | | |
| PT | New polypeptide comprising an extracellular domain of the transmembrane | |
| PT | activator and calcium-signal modulating cyclophilin ligand (CAML) | |
| PT | interactor (TACI), and a trimerizing polypeptide, useful for treating | |
| PT | inflammatory diseases. | |
| XX | | |
| XX | Example 4; SEQ ID NO 18; 36pp; English. | |
| PS | | |
| XX | The present invention describes an isolated polypeptide comprising an | |
| XX | extracellular domain of the transmembrane activator and calcium-signal | |
| CC | modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerizing | |
| CC | polypeptide. Also described: (1) a homotrimeric protein complex | |
| CC | comprising the polypeptide; (2) an expression vector comprising the | |
| CC | following operably linked elements, a transcription promoter, the nucleic | |
| CC | acid sequence encoding the polypeptide, and a transcription terminator; | |
| CC | (3) a cultured cell into which has been introduced the expression vector; | |
| CC | where the cell expresses the polypeptide; (4) producing a homotrimeric | |
| CC | protein complex by culturing the cell, and recovering the homotrimeric | |
| CC | protein complex; and (5) inhibiting tumour necrosis factor (TNF)/4-induced | |
| CC | B cell proliferation by exposing the B cells to the homotrimeric protein | |
| CC | complex. The polypeptide has antiinflammatory, antiarthritic, | |
| CC | antirheumatic, immunosuppressive, antiarteriosclerotic and cytostatic | |
| CC | activities, and can be used in gene therapy. The polypeptides are useful | |
| CC | for treating and controlling inflammatory diseases, e.g. rheumatoid | |
| CC | arthritis or inflammatory bowel disease, autoimmune disease, | |
| CC | atherosclerosis, osteoporosis, allograft rejection and cancer. The | |
| CC | present sequence represents a human TACI and heat shock binding protein | |
| CC | (HSBP) fusion protein fragment, which is used in the exemplification of | |
| CC | the present invention. | |
| XX | | |
| XX | Sequence 171 AA; | |
| SQ | | |
| | Query Match 33.1%; Score 66.5; DB 8; Length 171; | |
| | Best Local Similarity 32.4%; Pred. No. 1.7; | |
| | Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1 | |
| QY | 1 CSQNEYFDSLHACIPQCLRGSSNTPLTCQRYC 34 | |
| | : : : : : : : : | |
| DB | 6 CPBEQYWDPLLGTCWSCKTCIGNHQS-QRTCAFC 38 | |
| | : : : : : : : : | |
| RESULT 47 | | |
| AAE09244 | | |
| ID | AAE09244 standard; protein; 265 AA. | |
| XX | | |
| AC | AAE09244; | |
| XX | | |
| DT | 19-NOV-2001 (first entry) | |
| DE | Human TACI splice variant protein. | |
| XX | | |
| KW | Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; | |
| KW | TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; | |
| XX | autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis. | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200160397-Al. | |
| XX | | |
| PD | 23-AUG-2001. | |

PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.
 XX
 PS Disclosure; Fig 8; 153pp; English.
 XX
 CC The present sequence represents an alternatively spliced human TACI
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful
 CC for preparing a composition for treating systemic lupus erythematosus
 XX
 SQ Sequence 266 AA;

Query Match 33.1%; Score 66.5; DB 6; Length 266;
 Best Local Similarity 32.4%; Pred. No. 2.7; 14; Indels 1; Gaps 1;
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;
 QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCORYC 34
 Db 34 CPPEQYWDPLGLTGMSCCKTICNHQS-QRTCAAF 66

RESULT 49
 AAU10949
 ID AAU10949 standard; protein; 291 AA.
 XX
 AC AAU10949;

DT 12-MAR-2002 (first entry)

DE Human AGP-3 receptor extracellular domain.

XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; nontropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.

XX Homo sapiens.

XX WO200185782-A2.

XX 15-NOV-2001.

XX 12-FEB-2001; 2001WO-US004568.

XX 11-FEB-2000; 2000US-0181800P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Hsu H;

XX WPI; 2002-049441/06.

XX Composition, useful for identifying modulator of receptor for treating
 PT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor
 PT ligand family member) receptor and encoding nucleic acids.

XX Claim 1; Fig 18; 124pp; English.

XX The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumour necrosis factor ligand family member) related protein (II)
 CC attached to a vesicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds (agonists
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful

CC for identifying intracellular proteins that interact with the respective
 CC cytoplasmic domains by yeast two-hybrid screening process. (II) is
 CC involved in B cell growth, survival and activation particularly in lymph
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
 CC identified using (II) are used for modulating B cell response and are
 CC used to treat diseases characterised by inflammatory processes or
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-
 CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the
 CC production of hybridoma cells which are derived from B cells, which
 CC involves treating the hybridoma cells with (II). (II) is useful in the
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are
 CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,
 CC septic shock, etc. The nucleic acids are also useful for developing the
 CC transgenic animals expressing (II), which are useful for producing the
 CC polypeptides and for the study of in vivo biological activity. The
 CC present sequence represents the amino acid sequence of human AGP-3
 CC extracellular domain
 XX

SQ Sequence 291 AA;

Query Match 33.1%; Score 66.5; DB 5; Length 291;
 Best Local Similarity 32.4%; Pred. No. 2.9;
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCORYC 34
 Db 34 CPPEQYWDPLGLTGMSCCKTICNHQS-QRTCAAF 66

RESULT 50
 AAU75783

ID AAU75783 standard; protein; 293 AA.

XX AAU75783;

XX 18-JAN-1999 (first entry)

XX Human lymphocyte surface receptor TACI.

XX TACI; transmembrane activator and CAML-interactor;
 KW calcium signal-modulating cyclophilin ligand; human;
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
 KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
 KW immunosuppressive; graft versus host disease; transplant rejection;
 KW therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..166
 FT /label= Extracellular_domain
 FT /note= "Claim 8"
 FT Peptide 34..71
 FT /note= "TNFR_NGFR motif"
 FT Domain 167..186
 FT /label= Transmembrane_domain
 FT Domain 187..294
 FT /label= Cytoplasmic_domain
 FT /note= "Claim 6"

XX WO9839361-A1.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004270.

XX 03-MAR-1997; 97US-00810572.

(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

Bram RJ, Von Bulow G;

WPI; 1998-506346/43.

N-PSDB; AAV57328.

New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.

Claim 20; Fig 2a; 89pp; English.

This is the amino acid sequence of novel human transmembrane activator and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TACI is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targeted to specifically regulate B cell responses without affecting T cell activity. TACI cDNA (seeV57329) was isolated from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also claimed are the C-terminal (see AAW575784) and N-terminal (see AAW575785) fragments of TACI, recombinant DNA constructs, unicellular hosts, and antibodies to TACI protein. Methods are claimed for identifying a ligand for TACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes without affecting mature T lymphocytes. TACI can be activated to increase immune system activity, e.g. for treating infections or cancers. It can be blocked to provide immunosuppression, e.g. for treating autoimmune and inflammatory conditions such as immune complex- induced vasculitis, glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II collagen-induced arthritis, experimental allergic and hyperacute xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus, transplant rejection, cancer or graft versus host disease

Sequence 293 AA;

Query Match 33.1%; Score 66.5; DB 2; Length 293;

Query Match 33.1%; SCORE 86.5; D
Best Local Similarity 32.4%; Pred. No. 2.9;

Best Local Similarity 32.4%, Freq. NO. 2.5,
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

1 CSQNEYFDSLHLHACIPCQLRCSSTPPLTCQRYC 34
QY

34 CP E E Q Y W D P L L G T C M S C K T I C N H Q S - Q B T C A A F C 66

Search completed: January 28, 2005, 19:52:44

Job time : 39.3395 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:37:53 ; Search time 196.661 Seconds
(without alignments)
335.635 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964

Sequence: 1 MLQWAGCQSQNEYPDSLHA.....CKSLPAALSATREIKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_23Sep04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 964 | 100.0 | 184 | 3 AAB08843 | Aab08843 Amino aci |
| 2 | 964 | 100.0 | 184 | 3 AAY94001 | Aay94001 A human B |
| 3 | 964 | 100.0 | 184 | 4 AAE09241 | Aae09241 Human BCM |
| 4 | 964 | 100.0 | 184 | 4 AAY71979 | Aay71979 Human B C |
| 5 | 964 | 100.0 | 184 | 4 AAB60698 | Aab60698 Human BAF |
| 6 | 964 | 100.0 | 184 | 4 AAE00506 | Aae00506 Human B C |
| 7 | 964 | 100.0 | 184 | 5 ABB81487 | Abb81487 Human BCM |
| 8 | 964 | 100.0 | 184 | 5 ABB54694 | Abb54694 Metastati |
| 9 | 964 | 100.0 | 184 | 5 AAE28961 | Aae28961 Human B-C |
| 10 | 964 | 100.0 | 184 | 6 AAE35216 | Aae35216 Human B-C |
| 11 | 964 | 100.0 | 184 | 6 ADA49361 | Ada49361 Human BCM |
| 12 | 964 | 100.0 | 184 | 6 ABP60552 | Abp60552 Human tum |
| 13 | 964 | 100.0 | 184 | 6 ABP97717 | Abp97717 Amino aci |
| 14 | 964 | 100.0 | 184 | 7 ADD67527 | Add67527 Human Lyl |
| 15 | 964 | 100.0 | 184 | 7 ADG43715 | Adg43715 Human B-C |
| 16 | 964 | 100.0 | 184 | 8 ADK00756 | Adk00756 Native hu |
| 17 | 958 | 99.4 | 184 | 6 ABR40082 | Abr40082 Human Gen |
| 18 | 955 | 99.1 | 288 | 5 ABG95060 | Abg95060 Human tra |
| 19 | 950 | 98.5 | 181 | 5 AAE15484 | Aae15484 Human B-C |
| 20 | 719.5 | 74.6 | 157 | 4 AAB60700 | Aab60700 Human BAF |
| 21 | 572 | 59.3 | 185 | 3 AAB08844 | Aab08844 Amino aci |
| 22 | 572 | 59.3 | 185 | 4 AAY71980 | Aay71980 Murine B |
| 23 | 572 | 59.3 | 185 | 5 AAE15490 | Aae15490 Mouse B C |
| 24 | 323 | 33.5 | 58 | 5 AAE15501 | Aae15501 Human B C |
| 25 | 311.5 | 32.3 | 117 | 5 AAE15491 | Aae15491 Human-mur |

| | | | | | |
|----|-------|------|------|------------|--------------------|
| 26 | 286.5 | 29.7 | 302 | 4 AAB60699 | Aab60699 Mouse IgG |
| 27 | 286.5 | 29.7 | 302 | 4 AAE00507 | Aae00507 Human BCM |
| 28 | 286.5 | 29.7 | 302 | 4 ADG43717 | Adg43717 Human B-C |
| 29 | 286 | 29.7 | 283 | 5 AAE15488 | Aae15488 Human BCM |
| 30 | 284 | 29.5 | 51 | 5 AAE15485 | Aae15485 Human B-C |
| 31 | 201 | 20.9 | 34 | 5 AAE15486 | Aae15486 Human B-C |
| 32 | 201 | 20.9 | 34 | 6 ADA49366 | Ada49366 Human BCM |
| 33 | 187 | 19.4 | 281 | 6 AAE15489 | Aae15489 Mouse BCM |
| 34 | 158 | 16.4 | 42 | 6 ABJ38417 | Abj38417 TALL-1 re |
| 35 | 151 | 15.7 | 26 | 7 ADI53060 | Adi53060 Human BCM |
| 36 | 116.5 | 12.1 | 175 | 5 ABB78398 | Abb78398 Amino aci |
| 37 | 116.5 | 12.1 | 175 | 5 AAE22244 | Aae22244 Murine BA |
| 38 | 116.5 | 12.1 | 175 | 5 ABB81489 | Abb81489 Mouse Zcn |
| 39 | 116.5 | 12.1 | 175 | 6 ABP97722 | Abp97722 Amino aci |
| 40 | 106.5 | 11.0 | 185 | 5 AAE22266 | Aae22266 Human BAF |
| 41 | 105.5 | 10.9 | 185 | 5 AAE22267 | Aae22267 Human BAF |
| 42 | 104 | 10.8 | 21 | 5 AAE15487 | Aae15487 Human B-C |
| 43 | 103.5 | 10.7 | 185 | 5 AAE22269 | Aae22269 Human BAF |
| 44 | 100.5 | 10.4 | 185 | 5 AAE22271 | Aae22271 Human BAF |
| 45 | 100 | 10.4 | 185 | 7 ADB90663 | Adb90663 TALL-1R g |
| 46 | 99.5 | 10.3 | 185 | 5 AAE22268 | Aae22268 Human BAF |
| 47 | 97.5 | 10.1 | 185 | 5 AAE22270 | Aae22270 Human BAF |
| 48 | 94.5 | 9.8 | 185 | 5 AAE22242 | Aae22242 Human mat |
| 49 | 93 | 9.6 | 184 | 5 ABB81483 | Abb81483 Human Zcn |
| 50 | 93 | 9.6 | 184 | 6 AAE35227 | Aae35227 Human Zcn |
| 51 | 93 | 9.6 | 184 | 6 ADA49363 | Ada49363 Human BAF |
| 52 | 93 | 9.6 | 184 | 6 ABP97721 | Abp97721 Amino aci |
| 53 | 93 | 9.6 | 184 | 6 ABR61767 | Abr61767 Human PRO |
| 54 | 93 | 9.6 | 184 | 8 ADK00764 | Adk00764 Native hu |
| 55 | 93 | 9.6 | 266 | 5 AAE22243 | Aae22243 Human UST |
| 56 | 92.5 | 9.6 | 185 | 7 ABR82287 | Abr82287 Human BRO |
| 57 | 92.5 | 9.6 | 334 | 6 AAO29657 | Aao29657 Paederus |
| 58 | 91 | 9.4 | 171 | 7 ADB90668 | Adb90668 TALL-1R g |
| 59 | 91 | 9.4 | 171 | 7 ADB90665 | Adb90665 TALL-1R g |
| 60 | 90.5 | 9.4 | 24 | 5 AAE15492 | Aae15492 Human-mur |
| 61 | 90.5 | 9.4 | 170 | 7 ADB90667 | Adb90667 TALL-1R g |
| 62 | 86.5 | 9.0 | 392 | 6 AAE35223 | Aae35223 Human TAC |
| 63 | 86.5 | 9.0 | 867 | 7 ADG42639 | Adg42639 Mouse pro |
| 64 | 84 | 8.7 | 332 | 6 AAE35228 | Aae35228 Human TAC |
| 65 | 83.5 | 8.7 | 404 | 5 AAO14136 | Aao14136 Protein o |
| 66 | 83 | 8.6 | 348 | 6 AAE35225 | Aae35225 Human TAC |
| 67 | 82 | 8.5 | 1009 | 2 AAW48374 | Aaw48374 Mouse rel |
| 68 | 82 | 8.5 | 1009 | 2 AAW64568 | Aaw64568 Murine pr |
| 69 | 82 | 8.5 | 1009 | 2 AAW61196 | Aaw61196 Mouse pro |
| 70 | 81.5 | 8.5 | 186 | 7 ADB90675 | Adb90675 TALL-1R p |
| 71 | 81 | 8.4 | 576 | 2 AAY23925 | Aay23925 Amino aci |
| 72 | 80.5 | 8.4 | 441 | 8 ADJ10421 | Adj10421 DHBV Pres |
| 73 | 79.5 | 8.2 | 293 | 5 AAU09900 | Aau09900 Human AGP |
| 74 | 79.5 | 8.2 | 955 | 8 ADK71879 | Adk71879 Human Kin |
| 75 | 79.5 | 8.2 | 967 | 7 ADC99077 | Adc99077 Human KPP |
| 76 | 79.5 | 8.2 | 1009 | 2 AAR98351 | Aar98351 Probin ty |
| 77 | 79.5 | 8.2 | 1009 | 2 AAW48373 | Aaw48373 Human rel |
| 78 | 79.5 | 8.2 | 1009 | 2 AAW57891 | Aaw57891 Human PYK |
| 79 | 79.5 | 8.2 | 1009 | 6 ABU04900 | Abu04900 Human exp |
| 80 | 79.5 | 8.2 | 1009 | 6 ABU04903 | Abu04903 Human exp |
| 81 | 79.5 | 8.2 | 1009 | 6 ABU04898 | Abu04898 Human exp |
| 82 | 79.5 | 8.2 | 1009 | 6 ABU04899 | Abu04899 Human exp |
| 83 | 79.5 | 8.2 | 1009 | 6 ABU04902 | Abu04902 Human exp |
| 84 | 79.5 | 8.2 | 1009 | 6 ABU04901 | Abu04901 Human exp |
| 85 | 79.5 | 8.2 | 1009 | 6 ABU04897 | Abu04897 Human exp |
| 86 | 79.5 | 8.2 | 1009 | 6 ABU04896 | Abu04896 Human exp |
| 87 | 79.5 | 8.2 | 1009 | 7 ADF60991 | Adf60991 Pain asso |
| 88 | 79.5 | 8.2 | 1009 | 8 ADI57188 | Adi57188 Human FAK |
| 89 | 79.5 | 8.2 | 1009 | 8 ADJ75553 | Adj75553 Marker ge |
| 90 | 79.5 | 8.2 | 1009 | 8 ADP44083 | Adp44083 Human PTK |
| 91 | 79 | 8.2 | 857 | 2 AAR29814 | Aar29814 S recepto |
| 92 | 78.5 | 8.1 | 265 | 4 AAE09244 | Aae09244 Human TAC |
| 93 | 78.5 | 8.1 | 266 | 6 ABP97723 | Abp97723 Amino aci |
| 94 | 78.5 | 8.1 | 293 | 2 AAW75783 | Aaw75783 Human lym |
| 95 | 78.5 | 8.1 | 293 | 3 AAB36312 | Aab36312 Human neu |
| 96 | 78.5 | 8.1 | 293 | 3 AAY94000 | Aay94000 A transme |
| 97 | 78.5 | 8.1 | 293 | 4 AAE09240 | Aae09240 Human TAC |
| 98 | 78.5 | 8.1 | 293 | 4 AAY71914 | Aay71914 Human tum |

99 78.5 8.1 293 5 AAO14130 AAO14130 Human tra
100 78.5 8.1 293 5 ABB81488 ABB81488 Human TAC

ALIGNMENTS

RESULT 1
ID AAB08843 standard; peptide, 184 AA.
XX AAB08843;
XX
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of human.
XX
XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
XX anti-cell death gene; apoptosis; viral infection; inflammatory response;
XX rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Domain 57..77
XX /note= "putative transmembrane domain"

XX WO2000050633-A1.
XX 31-AUG-2000.
XX 24-FEB-2000; 2000WO-US004925.
XX 24-FEB-1999; 99US-0121485P.
XX (GHEO) GEN HOSPITAL CORP.
XX Seed B, Ting A;
XX WPI; 2000-558405/51.
XX
XX Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
XX gene and reporter gene, and determining alteration in reporter gene
XX expression.
XX
XX Claim 32; Fig 7A; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
XX a necrosis factor (NF)-kB activator. The method of the invention is used
XX to identify compounds which modulate BCMA activity (and thus NF-kB
XX activity). The specification describes a method of identifying a
XX polypeptide which increases gene expression from a promoter. The method
XX involves contacting a library of with a cell which expresses a
XX recombinant anti-cell death gene and a reporter gene operably linked to
XX the promoter, and then determining whether the expression of the reporter
XX gene is altered as a result of contact with library. The method is useful
XX for identifying polypeptides which increase or decrease gene expression
XX from a promoter. The BCMA polypeptide or nucleic acid are useful for
XX preparing a pharmaceutical composition for treating cancer, apoptosis,
XX viral infections, inflammatory response, such as rheumatoid arthritis,
XX inflammatory bowel disease or septic shock. BCMA is useful for
XX identifying compounds that modulate NF-kB expression and thus for drug
XX designing

XX SQ Sequence 184 AA;
XX
XX Query Match 100.0%; Score 964; DB 3; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-95;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQSQNEYFDSLLHACIPQLRCSSTNPPLTTCQRYCNASVTNSVKGTHAILWTCL 60

Db 1 MLQWAGQSQNEYFDSLLHACIPQLRCSSTNPPLTTCQRYCNASVTNSVKGTHAILWTCL 60
Qy 61 GLSLIIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGTDEIILPRGLE 120
Db 61 GLSLIIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSGTDEIILPRGLE 120
Qy 121 YTVEECTCEDCIKSPKVDSDHCHFPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVEECTCEDCIKSPKVDSDHCHFPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 2
AAY94001
ID AAY94001 standard; protein, 184 AA.
XX AAY94001;
XX
XX 20-OCT-2000 (first entry)
XX
XX A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

XX WO2000040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000396.

XX 07-JAN-1999; 99US-00226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX N-PSDB; AAA58559.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Disclosure; Page 152; 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
XX with activated or resting B lymphocytes, effector T-cells, or with
XX antibody production. The antibody production is associated with an
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
XX and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, end stage renal failure,

CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. B843x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Qy 61 GLSLIIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSGTDEIILPRGLE 120
 Db 61 GLSLIIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSGTDEIILPRGLE 120
 Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184

RESULT 3
 AAE09241
 ID AAE09241 standard; protein; 184 AA.

XX AC AAE09241;
 XX DT 19-NOV-2001 (first entry)
 XX DE Human BCMA protein.
 XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 OS Homo sapiens.
 XX W0200160397-Al.
 XX PD 23-AUG-2001:
 XX PF 28-NOV-2000; 2000WO-US032378.
 XX PR 16-FEB-2000; 2000US-0182938P.
 XX PR 22-AUG-2000; 2000US-0226986P.
 XX PA (GETH) GENENTECH INC.
 XX PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM,
 PI Yan M;
 XX WPI; 2001-541628/60.
 XX DR N-PSDB; AAD15902.
 XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.
 XX PS Example 2; Fig 2; 160pp; English.
 XX CC The invention relates to methods of using one or more agonists or

CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human BCMA protein
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTVSVKGTNAILWTCL 60
 Qy 61 GLSLIIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSGTDEIILPRGLE 120
 Db 61 GLSLIIISLAVFVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSGTDEIILPRGLE 120
 Qy 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVVEECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184

RESULT 4
 AAY71979
 ID AAY71979 standard; protein; 184 AA.

XX AC AAY71979;
 XX DT 28-MAR-2001 (first entry)
 XX DE Human B cell maturation factor (BCMA) protein.
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and ApOL-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX Domain 1..62
 XX FT /label= Extracellular_domain
 XX PN W0200068378-Al.
 XX PD 16-NOV-2000.
 XX PF 05-MAY-2000; 2000WO-US012266.
 XX PR 06-MAY-1999; 99US-0132892P.
 XX PR 01-MAY-2000; 2000US-0201012P.
 XX PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX PI Shu HS;
 XX DR WPI; 2001-016094/02.

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DR N-PSDB; AAD02125.
XX Isolated TALL-1 protein is used to identify compounds that regulate B
PT lymphocyte proliferation, used to treat B lymphocyte associated
PT autoimmune disorders.
XX
XX Claim 37; Page 104-105; 112pp; English.
XX
XX The present invention relates to Tumour necrosis factor (TNF) and Apol-
CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
CC proteins (including homologues), and their antibodies. The invention in
CC particular relates to methods for regulating the interaction between TALL
CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
CC TALL-1 protein is useful for identifying compounds that regulate B
CC lymphocyte proliferation. It is also useful for treating B lymphocyte
CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC glomerulonephritis, or polyarthritis nodosa. The TALL-1 protein and its
CC corresponding nucleic acid sequence are also useful in diagnostic assays.
CC The present sequence is a human B cell maturation factor (BCMA) protein.
CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
CC increases with B lymphocyte maturation
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 964; DB 4; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-95;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGKTNAILWTCL 60
XX 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGKTNAILWTCL 60
XX
XX 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSGTDEIILPGL 120
XX 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSGTDEIILPGL 120
XX
XX 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
XX 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
XX
XX 181 ISAR 184
XX 181 ISAR 184
XX
XX RESULT 5
XX AAB60698
XX ID AAB60698 standard; protein; 184 AA.
XX
XX AC AAB60698;
XX
XX XX 22-MAY-2001 (first entry)
XX
XX DE Human BAFF receptor (BAFF-R).
XX
XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor; BCMA;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX renal disorder; immunosuppressive disorder; HIV infection;
XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX lymphoma; gene therapy; cancer; tumour.
XX

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OS Homo sapiens.
XX WO200112812-A2.
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000WO-US022507.
XX
XX 17-AUG-1999; 99US-0149378P.
XX 11-FEB-2000; 2000US-0181684P.
XX 18-FEB-2000; 2000US-0183536P.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX WPI; 2001-202866/20.
XX N-PSDB; AAF59998.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAFF-receptor polypeptide,
XX chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
XX
XX Claim 20; Fig 1; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory
XX agent, and also plays a role in the development of hypertension and
XX related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
XX specific antibodies can be used for inhibiting B-cell growth, dendritic
XX cell-induced B-cell growth and maturation, and immunoglobulin production,
XX and in the treatment of autoimmune disorders, B-cell lymphoproliferative
XX disorders, hypertension and renal disorders. The BAFF-R proteins may also
XX be used in the treatment of immunosuppressive disorders and HIV
XX infection, and in patients undergoing organ transplantation. The BAFF-R
XX proteins or BAFF-R specific antibodies may be used for treating
XX suppressing or altering an immune response involving a signalling pathway
XX between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
XX inhibits B-cell growth and maturation it is useful for treating diseases
XX such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
XX Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
XX progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
XX human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
XX autoimmune disorders and inherited B-cell-associated disorders. The
XX present sequence represents human BAFF-R
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 964; DB 4; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-95;
XX Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGKTNAILWTCL 60
XX 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKGKTNAILWTCL 60
XX
XX 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSGTDEIILPGL 120
XX 61 GLSLIIISLAVFLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSGTDEIILPGL 120
XX
XX 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
XX 121 YTVSECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
XX
XX 181 ISAR 184
XX 181 ISAR 184
XX

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RESULT 6
AAE00506
ID AAE00506 standard; protein; 184 AA.
XX
AC AAE00506;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human B cell maturation protein (BCMA).
XX
KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF;
KW tumour necrosis factor; BCMA; B cell maturation protein.
XX
OS Homo sapiens.
XX
FN WO200124811-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027579.
XX
PR 06-OCT-1999; 99US-0157933P.
PR 11-FEB-2000; 2000US-0181807P.
PR 30-JUN-2000; 2000US-0215688P.
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.
XX
PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX
DR WPI; 2001-266242/27.
DR N-PSDB; AAD03844.
XX
XX
PT Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
PT antagonist.
XX
PS Claim 3; Fig 3A; 85pp; English.
XX
CC The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or carcinoma.
CC The method involves administering a composition comprising A
CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
CC maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and human
CC immunodeficiency virus (HIV), and for treating, suppressing or altering
CC an immune response involving a signalling pathway between APRIL-R and its
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
CC is human APRIL-R also referred as BCMA or BCM protein
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MLQWAGQCSNEYFDSLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKGTTNAILWTCL 60
Db 1 MLQWAGQCSNEYFDSLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKGTTNAILWTCL 60

Oy 61 GLSLIISLAVFLVLMFLLRKISSEPLKDEFFKNTSGLLGMANIDLEKSRGTGEIILPRGLE 120
Db 61 GLSLIISLAVFLVLMFLLRKISSEPLKDEFFKNTSGLLGMANIDLEKSRGTGEIILPRGLE 120
Oy 121 YTVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Oy 181 ISAR 184
Db 181 ISAR 184
RESULT 7
ABB81487
ID ABB81487 standard; protein; 184 AA.
XX
AC ABB81487;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human BCMA receptor related protein SEQ ID NO:7.
XX
KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.
XX
OS Homo sapiens.
XX
FN WO200238766-A2.
XX
PD 16-MAY-2002.
XX
PF 05-NOV-2001; 2001WO-US047018.
XX
PR 07-NOV-2000; 2000US-0246449P.
PR 20-DEC-2000; 2000US-0257131P.
PR 28-JUN-2001; 2001US-0301715P.
PR 29-AUG-2001; 2001US-0315565P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gross JA, Xu W, Henne RM, Grant FJ;
XX
DR WPI; 2002-508212/54.
XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
PS Disclosure; Page 135-136; 154pp; English.
XX
CC The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid

CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60

QY 61 GLSLIISLAVFLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTGDEIILPRGLE 120
 DB 61 GLSLIISLAVFLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTGDEIILPRGLE 120

QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180

QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 8
 ABP54694
 ID ABP54694 standard; protein; 184 AA.

XX AC ABP54694;
 XX DT 30-DEC-2002 (first entry)
 XX DE Metastatic colorectal cancer-associated polypeptide.
 XX KW Colorectal cancer; metastasis; differential expression; cytostatic;
 XX KW diagnosis; gene therapy; vaccine.
 XX OS Homo sapiens.
 XX PN WO200268677-A2.
 XX PD 06-SEP-2002.
 XX PF 27-FEB-2002; 2002WO-US006001.
 XX PR 27-FEB-2001; 2001US-0272206P.
 XX PR 02-APR-2001; 2001US-0281149P.
 XX PR 17-APR-2001; 2001US-0284555P.
 XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX FI Mack DH, Markowitz SD;
 XX DR WPI; 2002-698677/75.
 XX DR N-PSDB; ABQ81560.
 XX PT New genes that are up- or down-regulated in colorectal cancer, useful for
 PT diagnosing colorectal cancer in a subject, or for identifying modulators
 PT of colorectal cancer-associated proteins and genes for treating
 PT colorectal cancer.
 XX PS Claim 8; Page 255; 260pp; English.
 XX

CC The present sequence is the protein sequence of a human polypeptide
 CC encoded by a gene that exhibits decreased expression in colon cancer-
 CC derived metastases compared to normal colon tissue. It is an example of
 CC claimed polypeptides that are encoded by genes which are differentially
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are
 CC useful in diagnostic and prognostic assays, for raising antibodies useful
 CC e.g. in immunotherapy, and in screening for modulator compounds of
 CC therapeutic value
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASVTNSVKGTHAILWTCL 60

QY 61 GLSLIISLAVFLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTGDEIILPRGLE 120
 DB 61 GLSLIISLAVFLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTGDEIILPRGLE 120

QY 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 DB 121 YTVVECTCEDCIKSKPKVDSHCFPLPAMEBEGATILVTTKTNDYCKSLPAALSATEIEKS 180

QY 181 ISAR 184
 DB 181 ISAR 184

RESULT 9
 AAE28961
 ID AAE28961 standard; protein; 184 AA.

XX AC AAE28961;
 XX DT 27-JAN-2003 (first entry)
 XX DE Human B-cell maturation antigen (BCMA).
 XX KW Human; tumour; B-cell maturation antigen; transmembrane activator;
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 KW BCMA; multiple myeloma.
 XX OS Homo sapiens.
 XX PF Key Region Location/Qualifiers
 FT Region 1..54 /note= "Antigenic epitope"
 FT Domain 1..48 /note= "Extracellular domain"
 FT Region 8..41 /note= "Cysteine rich region"
 XX WO200266516-A2.
 XX PD 29-AUG-2002.
 XX PF 06-FEB-2002; 2002WO-US003500.
 XX PR 20-FEB-2001; 2001US-0270274P.
 XX PR 12-APR-2001; 2001US-0283447P.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Kindsvogel W;
 XX DR WPI; 2002-723183/78.
 XX DR N-PSDB; AAD46410.

XX B-cell maturation antigen and transmembrane activator and calcium-
 PT modulator and cyclophilin ligand-interactor, useful for treating
 PT disorders e.g. inflammation or lymphoma.
 XX
 XX Disclosure; Page 63; 67pp; English.
 PS
 XX The invention relates to the manufacture of a composition for inhibiting
 CC the proliferation of tumour cells. The method involves using an antibody
 CC component that binds both the B-cell maturation antigen (BCMA) and the
 CC transmembrane activator and calcium-modulator and cyclophilin ligand-
 CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
 CC for inhibiting proliferation of tumour cells, particularly inhibiting
 CC ZTNF4 activity in a mammal associated with increased endogenous antibody
 CC production or a disorder consisting of neoplasm, chronic lymphocytic
 CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
 CC lymphoproliferative disease or light chain gammopathy or inflammation
 CC e.g. asthma. The invention is also useful in gene therapy. The present is
 CC human BCMA protein
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLCRCSSNTPPLTCORYCNASVTSVKGNTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLHACIPQLCRCSSNTPPLTCORYCNASVTSVKGNTNAILWTCL 60
 Qy 61 GLSLIIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Qy 121 YTVEECTCEDCIKSKPKVDSHCHPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVEECTCEDCIKSKPKVDSHCHPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184
 RESULT 10
 AAE35216
 ID AAE35216 standard; protein; 184 AA.
 XX
 XX AAE35216;
 XX
 XX 28-MAY-2003 (first entry)
 XX
 XX Human B-cell maturation receptor (BCMA) protein.
 XX
 XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW B-cell maturation receptor; BCMA; receptor.
 XX
 XX Homo sapiens.
 XX
 XX WO200294852-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 20-MAY-2002; 2002WO-US015910.
 XX
 XX 24-MAY-2001; 2001US-0293343P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.

XX Rixon MW, Gross JA;
 XX WPI; 2003-148455/14.
 DR N-PSDB; AAD53754.
 XX
 XX Transmembrane activator and calcium modulator and cyclophilin ligand-
 PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
 PT diabetes, comprises a TACI receptor group and an immunoglobulin group.
 XX
 XX Disclosure; Col 100; 71pp; English.
 XX
 XX The invention relates to fusion proteins comprising transmembrane
 CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)
 CC receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
 CC ZTNF4; and an immunoglobulin group comprising a constant region of an
 CC immunoglobulin. The invention is used to manufacture a medicament for
 CC inhibiting the proliferation of tumour cells in a mammalian subject. The
 CC composition comprising the fusion protein may also be used in treating
 CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple
 CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
 CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
 CC rejection, anaemia and septic shock. The fusion proteins are also used in
 CC gene therapy. The present sequence is human B-cell maturation receptor
 CC (BCMA) protein used in the invention
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLQWAGQCSQNEYFDSLHACIPQLCRCSSNTPPLTCORYCNASVTSVKGNTNAILWTCL 60
 Db 1 MLQWAGQCSQNEYFDSLHACIPQLCRCSSNTPPLTCORYCNASVTSVKGNTNAILWTCL 60
 Qy 61 GLSLIIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Db 61 GLSLIIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSTGDEIILPRGLE 120
 Qy 121 YTVEECTCEDCIKSKPKVDSHCHPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db 121 YTVEECTCEDCIKSKPKVDSHCHPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qy 181 ISAR 184
 Db 181 ISAR 184
 RESULT 11
 ADA49361
 ID ADA49361 standard; protein; 184 AA.
 XX
 XX ADA49361;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Human BCMA protein.
 XX
 XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;
 KW antiinflammatory; antiarthritis; dermatological; antidiabetic;
 KW neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;
 KW vaccine; autoimmune disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; insulin dependent diabetes mellitus;
 KW multiple sclerosis; myasthenia gravis; Grave's disease;
 KW autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
 KW Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA.
 XX
 XX Homo sapiens.
 OS
 XX WO2003035846-A2.
 XX
 XX

PD 01-MAY-2003.
 XX
 PF 24-OCT-2002; 2002WO-US034376.
 XX
 PR 24-OCT-2001; 2001US-0345106P.
 PR 14-JAN-2002; 2002US-0348962P.
 PR 07-FEB-2002; 2002US-0354966P.
 PR 13-AUG-2002; 2002US-0403364P.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Zhang G, Shu H, Liu Y, Xu L;
 XX
 DR WPI; 2003-403345/38.
 DR N-PSDB; ADA49360.
 XX
 XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
 PT activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.
 XX
 PS Claim 62; Page 613; 618pp; English.
 XX
 PS The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting abqr; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipruritic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents human BCMA.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 QY 61 GLSLIIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 DB 61 GLSLIIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 QY 121 YTVVECTCEDCICKSPKVDSDHCPFLPAMEGATILVTTKTNDYCKSLPALSALEIEKS 180
 DB 121 YTVVECTCEDCICKSPKVDSDHCPFLPAMEGATILVTTKTNDYCKSLPALSALEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 12
 ID ABP60552
 AC ABP60552 standard; protein; 184 AA.
 XX
 XX ABP60552;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Human tumour necrosis factor BCMA.
 XX

KW APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 KW dermatologic; immunosuppressive; antiinflammatory; antirheumatic;
 KW antiarthritic; cytostatic; antianaemic; antiallergic; antidiabetic;
 KW neuroprotective; ophthalmological; tuberculosic; antidiabetic;
 KW antipeptidic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
 KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
 KW inflammatory disorder; proliferative disorder; single chain antibody;
 KW antibody; human; BCMA; tumour necrosis factor.
 XX
 OS Homo sapiens.
 XX
 XX WO200294192-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 22-MAY-2002; 2002WO-US016106.
 XX
 XX 24-MAY-2001; 2001US-0293100P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM;
 XX
 XX WPI; 2003-156740/15.
 XX
 XX Novel isolated antibody that immunospecifically binds tumour necrosis
 PT factor delta, useful for treating, preventing or ameliorating Non-
 PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 PT syndrome.
 XX
 XX Disclosure; Page 222; 225pp; English.
 XX
 XX The invention relates to a novel antibody or its fragment, which
 CC immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
 CC The antibody of the invention has dermatological, immunosuppressive,
 CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
 CC antiallergic, antidiabetic, neuroprotective, ophthalmological,
 CC tuberculosic, antidiabetic, antipsoriatic, anti-HIV,
 CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
 CC The antibody or its fragment are useful for treating, preventing or
 CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 CC human, disease or disorder such as autoimmune disease, and graft versus
 CC host disease (GVHD). The autoimmune disease is systemic lupus
 CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
 CC is useful for detecting, diagnosing, prognosing, treating, preventing or
 CC ameliorating a disease or disorder associated with aberrant APRIL or
 CC APRIL receptor expression or aberrant function of APRIL or APRIL
 CC receptor. The disease or disorders includes autoimmune and inflammatory
 CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
 CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
 CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
 CC system, particularly B cell cancers, immune disorders such as myasthenia
 CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
 CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
 CC proliferative disorders (e.g. leukemia). The present sequence represents
 CC the tumour necrosis factor BCMA
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 964; DB 6; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.7e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGNTAILWTCL 60
 QY 61 GLSLIIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 DB 61 GLSLIIISLAVFLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
 QY 121 YTVVECTCEDCICKSPKVDSDHCPFLPAMEGATILVTTKTNDYCKSLPALSALEIEKS 180
 DB 121 YTVVECTCEDCICKSPKVDSDHCPFLPAMEGATILVTTKTNDYCKSLPALSALEIEKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184

Db 121 YTVECTCECIKSPKVDSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
181 ISAR 184
Db 181 ISAR 184

RESULT 13
ID ABP97717 standard; protein; 184 AA.
AC ABP97717;
XX 28-MAY-2003 (first entry)
DT XX
DE Amino acid sequence of human BCMA receptor.
XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus; BCMA.
XX Homo sapiens.
OS
XX WO2003014294-A2.
PN
XX 20-FEB-2003.
PD
XX 24-JUL-2002; 2002WO-US023487.
XX
XX 03-AUG-2001; 2001US-0310114P.
PR
XX 30-APR-2002; 2002US-0377171P.
PR
XX (GETH) GENENTECH INC.
PA
XX
XX Dixit V, Grewal I, Ridgway J, Yan M;
PI
XX WPI; 2003-256560/25.
XX
XX N-PSDB; ABZ68871.
DR
XX
XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.
PT
XX
XX Disclosure; Fig 2; 153pp; English.
PS
XX
XX The present sequence represents a human BCMA polypeptide. The
CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
CC preparing a composition for treating systemic lupus erythematosus
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLOWAGCQSNVEYFDSLHACIPQALRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLOWAGCQSNVEYFDSLHACIPQALRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120
Qy 121 YTVECTCECIKSPKVDSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVECTCECIKSPKVDSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 14
ADD67527
ID ADD67527 standard; protein; 184 AA.
XX
XX ADD67527;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX Human Ly1732P protein SEQ ID NO:4.
DE
XX
XX haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
KW vaccine; immunotherapy; cancer; multiple myeloma cell;
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
KW human.
XX
XX Homo sapiens.
OS
XX WO2003062401-A2..
PN
XX 31-JUL-2003.
PD
XX
XX 22-JAN-2003; 2003WO-US002353.
XX
XX 22-JAN-2002; 2002US-00057475.
PR
XX (CORI-) CORIXA CORP.
PA
XX Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
XX Carter L, Mcneill PD;
PI
XX WPI; 2003-598749/56.
XX
XX N-PSDB; ADD67526.
DR
XX
XX New hematological malignancy-related genes and polypeptides, useful for
PT screening anti-cancer agents, and generating antibodies or
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic
PT lymphocytic leukemia.
PT
XX
XX Claim 9; SEQ ID NO 4; 307pp; English.
PS
XX
XX The present invention describes an isolated polynucleotide (I), which is
CC overexpressed in haematological malignancies, and which encodes a
CC polypeptide or an immunogenic fragment of the polypeptide. Also
CC described: (1) an isolated polypeptide; (2) an expression vector
CC comprising (I) operably linked to an expression control sequence; (3) a
CC host cell comprising an expression vector; (4) an isolated antibody that
CC specifically binds to the polypeptide or its immunogenic fragment; and
CC (5) immunoconjugates comprising the antibody above, or an antibody that
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded
CC by (I). (I) has cytostatic and immunostimulant activities, and can be
CC used in vaccines and immunotherapy. The immunoconjugates are useful in
CC the manufacture of a medicament, particularly as active ingredients in a
CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.
CC The polynucleotide (I) or polypeptide can be used for screening anti-
CC cancer agents, and generating antibodies or immunoconjugates for treating
CC or preventing the above-mentioned diseases. The polynucleotide,
CC polypeptide or antibody can be used for detecting, diagnosing or
CC prognosticating the haematological malignancies described above. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLOWAGCQSNVEYFDSLHACIPQALRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
Db 1 MLOWAGCQSNVEYFDSLHACIPQALRCSSNTPPLTCQRYCNASVTNSVKGTHAILWTCL 60
Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTDEIILPRGLE 120

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
QY 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
Db 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

RESULT 15
ADG43715
ID ADG43715 standard; protein; 184 AA.
XX
AC ADG43715;
DT 26-FEB-2004 (first entry)
XX Human B-cell maturation antigen SEQ ID NO:1.
XX human; neurodegenerative immunological disorder; demyelination;
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003072713-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005147.
XX
PR 21-FEB-2002; 2002US-0358427P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Kalled SL, Reid H;
XX
DR WPI; 2003-721758/68.
DR N-PSDB; ADG43716.
XX
XX Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
PS Claim 8; Page 68-69; 72pp; English.
XX
XX The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, nontropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
XX inflammation. The present sequence represents human BCMA.
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 7; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQLCRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQLCRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60
QY 61 GLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDFKNTGSGLLGMANIDLEKSGRTGDEIILPRGLE 120
QY 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
Db 121 YTVSECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYCKSLPAALSATEIEKS 180
QY 181 ISAR 184
Db 181 ISAR 184

RESULT 16
ADK00756
ID ADK00756 standard; protein; 184 AA.
XX
AC ADK00756;
DT 06-MAY-2004 (first entry)
XX Native human BCMA.
XX
XX CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
KW Antibacterial; antiparasitic; systemic lupus erythematosus;
KW diabetes mellitus; AIDS; BCMA.
XX
OS Homo sapiens.
XX
PN WO2004011611-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023421.
XX
PR 25-JUL-2002; 2002US-0398530P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chuntharapai A, Grewal I, Kim KJ, Yan M;
XX
DR WPI; 2004-143841/14.
DR N-PSDB; ADK00755.
XX
XX New anti-TACI receptor monoclonal antibody, useful for diagnosing and
PT treating pathological conditions associated with tumor necrosis factor,
PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; SEQ ID NO 6; 110pp; English.
XX
XX The present invention relates to an isolated monoclonal antibody which
CC binds to a transmembrane activator of and CAML interactor (TACI)
CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI
CC polypeptide biological activity in mammalian cells, or for diagnosing and
CC treating pathological conditions associated with TNF and TNF receptor-
CC related molecules, e.g. cancer or immune-related disease, such as
CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
CC systemic vasculitis, diabetes mellitus, Crohn's disease,
CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or
CC infectious diseases including AIDS, hepatitis infection, bacterial
CC infection, fungal infection, protozoal infection and parasitic infection.
CC The present sequence represents native human BCMA.
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 8; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.7e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQLCRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQLCRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRLGLE 120
Db 61 GLSLIIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRLGLE 120
Qy 121 YTVVECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
Db 181 ISAR 184
RESULT 17
ID ABR40082 standard; protein; 184 AA.
XX ABR40082;
AC
DT 27-JUN-2003 (first entry)
XX Human Genoxit.
XX Human; genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant;
KW antidiabetic; hypotensive; ophthalmological; neuroprotective;
KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
KW Type III transmembrane protein; insulin resistance; atherosclerosis;
KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;
KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 1..54
FT /label= Extracellular_domain
FT Misc-difference 3
FT /label= Gln, Lys
FT Domain 55..77
FT /label= Transmembrane_domain
FT Domain 78..184
FT /label= Intracellular_domain
XX
FN WO2003013582-A1.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-IB003498.
XX
XX 06-AUG-2001; 2001US-0310754P.
XX (GSEST) GENSET SA.
XX
XX Lucas J, Dialynas D, Briggs K;
XX
XX WPI; 2003-268160/26.
XX N-PSDB; ACC00340.
XX
XX New use of agonist or antagonist of Genoxit activity for preventing or
XX treating obesity-related diseases or disorders, e.g. hyperlipidemia and
XX atherosclerosis.
XX
XX Disclosure; Page 32; 35pp; English.
XX
XX The present invention relates to the use of an agonist or antagonist of
XX Genoxit activity for preventing or treating obesity. Genoxit is a member
XX of the Tumour Necrosis Factor Receptor Super Family and is a Type III
XX transmembrane protein. The agonists or antagonists of the invention are
XX useful for treating or preventing obesity-related diseases or disorders,
XX e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
XX heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
XX blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
XX (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic

CC complications, e.g. microangiopathic lesions, ocular lesions,
CC retinopathy, neuropathy and renal lesions
XX
SQ Sequence 184 AA;
Query Match 99.4%; Score 958; DB 6; Length 184;
Best Local Similarity 99.5%; Pred. No. 4.3e-94;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCORYCNASVTVSKGTNAILWTCL 60
Db 1 MLXWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCORYCNASVTVSKGTNAILWTCL 60
Qy 61 GLSLIIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRLGLE 120
Db 61 GLSLIIISLAVFVLMFLRKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRLGLE 120
Qy 121 YTVVECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVVECTCEDCIKSKPKVDSHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy 181 ISAR 184
Db 181 ISAR 184
RESULT 18
ABG95060
ID ABG95060 standard; protein; 288 AA.
XX ABG95060;
AC
XX
XX 04-DEC-2002 (first entry)
XX Human translocation (4; 16)(q26; p13) protein.
XX Chromosome aberration; oncogenic fusion protein; cancer;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US006518.
XX
XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX N-PSDB; ABS73235.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX Disclosure; Page 189-190; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogenous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein

CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. hematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents a protein encoded by the DNA sequence of a
 CC chromosome aberration

XX SQ Sequence 288 AA;

Query Match 99.1%; Score 955; DB 5; Length 288;
 Best Local Similarity 99.5%; Pred. No. 1.6e-93;
 Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LOMAGQCSQNEYFSLHACIPQQLRCSSTPPLTCQRYCNASVTNSVKGTFNAILWTCLG 61
 Db 106 LKMGAGQCSQNEYFSLHACIPQQLRCSSTPPLTCQRYCNASVTNSVKGTFNAILWTCLG 165
 Qy 62 LSLIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRDGIILPRGLE 121
 Db 166 LSLIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRDGIILPRGLE 225
 Qy 122 TVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTNTNDYCKSLPAALSATEIEKSI 181
 Db 226 TVECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTNTNDYCKSLPAALSATEIEKSI 285
 Qy 182 SAR 184
 Db 286 SAR 288

RESULT 19
 AAE15484
 ID AAE15484 standard; protein; 181 AA.

XX AC AAE15484;

XX DT 12-MAR-2002 (first entry)

XX DE Human B-cell maturation (BCMA) protein.

XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 5..38

XX FT /note= "Cysteine-rich consensus region; This is region is
 specifically claimed as SEQ ID NO: 7 in claim 1 of the
 specification"

XX FT 52..72

XX FT /label= Transmembrane_domain

XX PN WO200187979-A2.

XX PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US015567.

XX PR 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX PA (AMGE-) AMGEN INC.

XX PI Theill LE, Yu G;

XX DR WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane
 XX activator and intracellular cyclophilin ligand interactor, by
 XX administering a binding partner for APRIL, a tumor necrosis factor family
 XX ligand.

XX PS Disclosure; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 XX activator and intracellular CAML interactor) and/or B cell maturation
 XX protein (BCMA) activity in a mammal. The method comprises administering a
 XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
 XX BCMA extracellular consensus sequence, but not the extracellular region
 XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
 XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 XX lymphoproliferative disorders, one or more solid tumours such as lung,
 XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 XX antagonists are useful for treating inflammation and immune function
 XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 XX disease), drug and insect sting allergy, inflammatory bowel disease
 XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 XX with leucocyte infiltration of the skin or organs. The present sequence
 XX is human BCMA protein

XX SQ Sequence 181 AA;

Query Match 98.5%; Score 950; DB 5; Length 181;

Best Local Similarity 100.0%; Pred. No. 3e-93;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSQNEYFDSLHACIPQQLRCSSTPPLTCQRYCNASVTNSVKGTFNAILWTCLG 63

Db 1 MAGQCSQNEYFDSLHACIPQQLRCSSTPPLTCQRYCNASVTNSVKGTFNAILWTCLG 60

Qy 64 LIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRDGIILPRGLE 123

Db 61 LIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRDGIILPRGLE 120

Qy 124 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTNTNDYCKSLPAALSATEIEKSI 183

Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTNTNDYCKSLPAALSATEIEKSI 180

Qy 184 R 184

Db 181 R 181

RESULT 20
 AAB60700

ID AAB60700 standard; protein; 157 AA.

XX AC AAB60700;

XX DT 22-MAY-2001 (first entry)

XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
 XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

immune-related disorder; B-cell growth inhibitor; BCMA;
 B-cell maturation inhibitor; immunoglobulin production inhibitor;
 autoimmunity disorder; B-cell lymphoproliferative disorder; hypertension;
 renal disorder; immunosuppressive disorder; HIV infection;
 organ transplantation; anti-inflammation; systemic lupus erythematosus;
 autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 lymphoma; gene therapy; cancer; tumour; plasmid pU535.
 Homo sapiens.
 WO200112812-A2.
 22-FEB-2001.
 16-AUG-2000; 2000WO-US022507.
 17-AUG-1999; 99US-0149378P.
 11-FEB-2000; 2000US-0181684P.
 18-FEB-2000; 2000US-0183536P.
 (BIOJ) BIOGEN INC.
 (APOT-) APOTEC R & D SA.
 Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 Thompson J;
 WPI; 2001-202866/20.
 N-PSDB; AAF60000.
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 lympho-proliferative disorder by administering BAFF-receptor polypeptide,
 chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 Example 1; Fig 3; 59pp; English.
 The invention relates to the use of a BAFF receptor (BAFF-R, also known
 as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 treatment of a variety of immune-related disorders. BAFF-R is a member of
 the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 agent, and also plays a role in the development of hypertension and
 related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 specific antibodies can be used for inhibiting B-cell growth, dendritic
 cell-induced B-cell growth and maturation, and immunoglobulin production,
 and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 disorders, hypertension and renal disorders. The BAFF-R proteins may also
 be used in the treatment of immunosuppressive disorders and HIV
 infection, and in patients undergoing organ transplantation. The BAFF-R
 proteins or BAFF-R specific antibodies may be used for treating,
 suppressing or altering an immune response involving a signalling pathway
 between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 inhibits B-cell growth and maturation it is useful for treating diseases
 such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 autoimmune disorders and inherited B-cell-associated disorders. The
 present sequence represents a human BAFF-R protein sequence as encoded by
 plasmid pU535. However, this BAFF-R protein sequence is 27 amino acids
 shorter than that given in AAB60698
 Sequence 157 AA;
 Query Match 74.6%; Score 719.5; DB 4; Length 157;
 Best Local Similarity 85.3%; Pred. No. 1.2e-68;
 Matches 157; Conservative 0; Mismatches 0; Indels 27; Gaps 9;
 1 MLOWAGCSQNEYFDSLLHACIPQLRCSSTPLTCORYCNASVTNSVGTNAILWTCL 60
 1 MLOWAGCSQNEYFDSLLHACIPQLRCSSTPLTCORYCNASVTN---GTNAILWTCL 51
 61 GLSLIIISLAVFLMFLRKISSEPLKDEFRKNTGSGLLGMANIDLEKSGRTGDEILPRGLE 120
 Db 1 MLOWAGCSQNEYFDSLLHACIPQLRCSSTPLTCORYCNASVTN---GTNAILWTCL 51
 Query Match 59.3%; Score 572; DB 3; Length 185;
 Best Local Similarity 62.6%; Pred. No. 9.6e-53;
 52 GLSLIIISLAVFLMFLRKISSEPLKDEFRKNTGSGLLGMANIDLEKSGRTGDEILPRGLE 102
 121 YTVBECTCEDCIKSPKVDSDHCFPPAPMBEGATILVTTNTNDYCKSLPALSALETEKS 180
 103 YTVBECT---CIKSPKVDSDHCFPLP---EGATILVTTNTNDYCKS---ALSATEIEKS 153
 181 ISAR 184
 154 ISAR 157
 RESULT 21
 AAB08844
 ID AAB08844 standard; peptide; 185 AA.
 XX AAB08844;
 AC AC
 DT 02-JAN-2001 (first entry)
 XX Amino acid sequence of murine BCMA polypeptide.
 DE BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX Mus musculus.
 OS XX
 FH Key Location/Qualifiers
 FT Domain 47..72
 FT /note= "putative transmembrane domain"
 XX WO200050633-A1.
 XX 31-AUG-2000.
 XX 24-FEB-2000; 2000WO-US004925.
 XX 24-FEB-1999; 99US-0121485P.
 XX (GCHO) GEN HOSPITAL CORP.
 XX Seed B, Ting A;
 XX WPI; 2000-558405/51.
 DR Identifying a modulator of gene expression for drug designing, by
 XX contacting a compound library with a cell expressing an anti-cell death
 XX gene and reporter gene, and determining alteration in reporter gene
 XX expression.
 XX Claim 32; Fig 7B; 53pp; English.
 XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
 XX a necrosis factor (NF)-kB activator. The method of the invention is used
 XX to identify compounds which modulate BCMA activity (and thus NF-kB
 XX activity). The specification describes a method of identifying a
 XX polypeptide which increases gene expression from a promoter. The method
 XX involves contacting a library of with a cell which expresses a
 XX recombinant anti-cell death gene and a reporter gene operably linked to
 XX the promoter, and then determining whether the expression of the reporter
 XX gene is altered as a result of contact with library. The method is useful
 XX for identifying polypeptides which increase or decrease gene expression
 XX from a promoter. The BCMA polypeptide or nucleic acid are useful for
 XX preparing a pharmaceutical composition for treating cancer, apoptosis,
 XX viral infections, inflammatory response, such as rheumatoid arthritis,
 XX inflammatory bowel disease or septic shock. BCMA is useful for
 XX identifying compounds that modulate NF-kB expression and thus for drug
 XX designing
 XX Sequence 185 AA;
 SQ

| | |
|-----------|---|
| CC | anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, |
| CC | pemphigus vulgaris, acute rheumatic fever, post-streptococcal |
| CC | glomerulonephritis, or polyarthritis nodosa. The TALL-1 protein and its |
| CC | corresponding nucleic acid sequence are also useful in diagnostic assays. |
| CC | The present sequence is a murine B cell maturation factor (BCMA). BCMA is |
| CC | the receptor for TALL-1 protein |
| XX | |
| XX | Sequence 185 AA; |
| SQ | |
| | Query Match 59.3%; Score 572; DB 4; Length 185; |
| | Best Local Similarity 62.6%; Pred. No. 9.6e-53; |
| | Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4; |
| QY | 4 MAGQCQNEYFDSLLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKGNTNAILWTCIGLS 63 |
| DB | 1 MAQCQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSPVTSSVKGTYTVLWIFLGLT 58 |
| QY | 64 LIISLAVFVLMFLRKISSEPLKDEPKN----TGSLLGWNATDLEKSRGTGEIILLPRGL 119 |
| DB | 59 LVLSTALFTISFLRKNPEALKDEQSPQQLDGSQAQLDKADTELTRIRAGDDRIFFPSRL 118 |
| QY | 120 EYTVSECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKNDYCK-SLPAAL-SATEI 177 |
| DB | 119 EYTVSECTCEDCVKSPKGDSDHFFPLPAMEEGATILVTTKGDYKSSVPTALQSVGM 178 |
| QY | 178 EKSISAR 184 |
| DB | 179 EKPTHTR 185 |
| RESULT 23 | |
| AAE15490 | |
| XX | ID AAE15490 standard; protein; 185 AA. |
| AC | AAE15490; |
| XX | |
| XX | 12-MAR-2002 (first entry) |
| XX | |
| XX | Mouse B cell maturation (BCMA) protein. |
| XX | |
| KW | Mouse; transmembrane activator and intracellular CAML interactor; TACI; |
| KW | cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; |
| KW | lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; |
| KW | prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; |
| KW | drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; |
| KW | Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; |
| KW | human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; |
| KW | rheumatoid arthritis; atherosclerosis. |
| OS | Mus sp. |
| OS | |
| PN | WO200187979-A2. |
| XX | |
| PD | 22-NOV-2001. |
| XX | |
| XX | 14-MAY-2001; 2001WO-US015567. |
| XX | |
| PR | 12-MAY-2000; 2000US-0204039P. |
| PR | 27-JUN-2000; 2000US-0214591P. |
| XX | 14-MAY-2001; 2001US-00214591. |
| XX | |
| PA | (AMGE-) AMGEN INC. |
| PI | Theill LE, Yu G; |
| XX | |
| XX | WPI; 2002-066696/09. |
| XX | |
| PT | Inhibiting activity of B cell maturation protein and/or transmembrane |
| PT | activator and intracellular cyclophilin ligand interactor, by |
| PT | administering a binding partner for APRIL, a tumor necrosis factor family |
| PT | ligand. |
| PS | Disclosure; Fig 11; 94pp; English. |

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein
 XX
 SQ Sequence 185 AA;
 Query Match 59.3%; Score 572; DB 5; Length 185;
 Best Local Similarity 62.6%; Pred. No. 9.6e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
 QY 4 MAGQCSNEYFDSLHACIPQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCLGLS 63
 DB 1 MAQCQFSEYFDSLHACKPCHLCSN--PATCQPCDPSVTSVKGTTVTLWIFLGLT 58
 QY 64 LIISLAVFVLMFLRKISSEPLKDFKN----TGSLLGMANIDLEKSRGDEILPRGL 119
 DB 59 LVLSLALFTISFLRKWNPEALKDEPQSPGLDGSQAQDKADTELTRAGDDRIFFPSL 118
 QY 120 EYTVECTCEDCIKSKVSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 DB 119 EYTVECTCEDCVKSKPGSDHFFPLPAMEEGATILVTTKTGDYKSSVPTALQSYVMGM-178
 QY 178 EKISAR 184
 DB 179 EKPTHTR 185
 RESULT 24
 AAEL15501
 ID AAEL15501 standard; peptide; 58 AA.
 AC AAEL15501;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B cell maturation protein cysteine rich extracellular region.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US015567.
 XX
 XX 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.
 XX (AMGE-) AMGEN INC.
 PA Theill LE, Yu G;
 PI WPI; 2002-066686/09.
 DR
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX
 PS Disclosure; Fig 13; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region
 XX
 SQ Sequence 58 AA;
 Query Match 33.5%; Score 323; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 9.9e-27;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCLGLSLI 65
 DB 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYCNASVTSVKGTTNAILWTCLGLSLI 58
 RESULT 25
 AAEL15491
 ID AAEL15491 standard; protein; 117 AA.
 AC AAEL15491;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)
 XX
 DE Human-murine B cell maturation protein (BCMA) consensus sequence.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; mouse.
 XX
 OS Homo sapiens.
 OS Mus' sp.
 OS Chimeric.
 XX
 XX WO200187979-A2.
 XX
 PD 22-NOV-2001.


```

Qy 61 GLSLIISLAVFLMFLRLKISSEPLKDFEKNYSGLLGMANIDLEKSTGDEIILPGCLE 120
Db 82 -----PPC-----PAPELLGGPSVFLFPPPKPKDTLMISRTPE 113
Qy 121 YTVBECTCEDCIKSPKVDSD-----HCFPLPAMEE-----GATILVTTKNDY-- 164
Db 114 VT---CVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNL 170
Qy 165 -----CKSLPAALSATEIEKIS 182
Db 171 GKEYCKVSNKALPA-PIEKTIS 192

RESULT 27
AAE00507
ID AAE00507 standard; protein; 302 AA.
XX
AC AAE00507;
XX
DT 11-SEP-2003 (revised)
DT 31-JUL-2001 (first entry)
XX
DE Human BCMA-Immunoglobulin G Fc region fusion construct.
XX
KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
KW immunoglobulin G; IgG; Fc region.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
FH Key
FT Protein
FT 1. .22
FT /label= Signal peptide
FT /note= "Derived from murine Ig kappa sequence"
FT
FT Protein
FT 23. .302
FT /label= Mature human_BCMA-IgG_Fc_fusion_protein
FT 23. .75
FT /note= "Derived from human BCMA protein"
FT
FT Domain
FT 24. .302
FT /label= Cysteine rich domain
FT /note= "Derived from human BCMA"
FT 76. .302
FT /note= "Derived from human IgG Fc region"
FT
XX WO200124811-A1.
XX
PD 12-APR-2001.
XX
XX
XX 05-OCT-2000; 2000WO-US027579.
XX
XX 06-OCT-1999; 99US-0157933P.
XX 11-FEB-2000; 2000US-0181807P.
XX 30-JUN-2000; 2000US-0215688P.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTECH R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX WPI; 2001-266242/27.
XX N-PSDB; AAD03847.
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
XX antagonist.

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XX Example 1; Fig 3B; 85pp; English.
XX
CC The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or carcinoma.
CC The method involves administering a composition comprising A
CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
CC maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and human
CC immunodeficiency virus (HIV), and for treating, suppressing or altering
CC an immune response involving a signalling pathway between APRIL-R and its
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
CC is a fusion construct containing human APRIL-R also referred as BCMA or
CC BCM protein, Fc region of human immunoglobulin G (IgG) and a signal
CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 302 AA;
Query Match 29.7%; Score 286.5; DB 4; Length 302;
Best Local Similarity 39.9%; Pred. No: 7e-22;
Matches 81; Conservative 13; Mismatches 54; Indels 55; Gaps 8;
Qy 1 MLQWAGCQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Db 24 MLQWAGCQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGVDK-THTC- 81
Qy 61 GLSLIISLAVFLMFLRLKISSEPLKDFEKNYSGLLGMANIDLEKSTGDEIILPGCLE 120
Db 82 -----PPC-----PAPELLGGPSVFLFPPPKPKDTLMISRTPE 113
Qy 121 YTVBECTCEDCIKSPKVDSD-----HCFPLPAMEE-----GATILVTTKNDY-- 164
Db 114 VT---CVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNL 170
Qy 165 -----CKSLPAALSATEIEKIS 182
Db 171 GKEYCKVSNKALPA-PIEKTIS 192

RESULT 28
ADG43717
ID ADG43717 standard; protein; 302 AA.
XX
AC ADG43717;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human B-cell maturation antigen-Fc SEQ ID NO:3.
XX
KW human; neurodegenerative immunological disorder; demyelination;
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;
KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;
KW gene therapy; mouse.
XX
OS Chimeric.
OS Homo sapiens.
OS Mus sp.
XX
FH Key
FT Location/Qualifiers
FT 1. .23
FT /note= "Murine IgGkappa signal sequence"
FT
FT Region
FT 24. .74
FT /note= "Human BCMA extracellular domain"
FT
FT Region
FT 75. .302
FT /note= "Human Ig heavy chain Fc region"
FT

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XX WO2003072713-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005147.
XX
XX 21-FEB-2002; 2002US-0358427P.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Kalled SL, Reid H;
XX
XX WPI; 2003-721758/68.
XX
XX N-PSDB; ADG43718.
XX
XX
XX Treating a neurodegenerative immunological disorder, e.g. demyelination
XX or inflammation in a mammal comprises administering a B-cell maturation
XX antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX
XX Claim 12; Page 70-71; 72pp; English.
XX
XX The invention relates to a novel method for treating a neurodegenerative
XX immunological disorder, demyelination or Central Nervous System (CNS)
XX inflammation in a mammal. The method comprises administering B-cell
XX maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
XX (the mammal has or is at risk of developing multiple sclerosis). The
XX method of the invention has neuroprotective, neurotropic, and
XX antiinflammatory activity, and may have a use in gene therapy. The
XX methods, BCMA, and antibodies are useful for treating a neurodegenerative
XX immunological disorder such as multiple sclerosis, demyelination or CNS
XX inflammation. The present sequence is used in the exemplification of the
XX invention.
XX
XX SQ Sequence 302 AA;
XX
XX Query Match 29.7%; Score 286.5; DB 7; Length 302;
XX Best Local Similarity 39.9%; Pred. No. 7e-22;
XX Matches 81; Conservative 13; Mismatches 54; Indels 55; Gaps 8;
XX
XX 1 MLQWAGQSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGKTNAILWTCL 60
XX 24 MLQWAGQSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGVDK-THTC- 81
XX
XX 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGEIILPRGLE 120
XX 82 -----PPC-----PAPELLGGPSVFLFPPKPKDTLMISRTPE 113
XX
XX 121 YTVBECTEDCIKSKPKVDS-----HCFPLPAMEE-----GATILVTTKNDY-- 164
XX 114 VT---CVVVDVSHEDPEVKFNWYDVGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLN 170
XX
XX 165 -----CKSLPALSALETEKSIS 182
XX 171 GKVKYKVSNNKALPA-PIEKTIS 192
XX
XX RESULT 29
XX AAE15488
XX ID AAE15488 standard; protein; 283 AA.
XX
XX AC AAE15488;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human BCMA-immunoglobulin Fc region fusion protein.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
```

```
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; fusion protein.
XX Homo sapiens.
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
XX 14-MAY-2001; 2001US-00214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor family
XX ligand.
XX
XX Disclosure; Fig 10B; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a
XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein-immunoglobulin Fc region fusion protein
XX
XX SQ Sequence 283 AA;
XX
XX Query Match 29.7%; Score 286; DB 5; Length 283;
XX Best Local Similarity 37.6%; Pred. No. 7.3e-22;
XX Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;
XX
XX 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGKTNAILWTCLGLS 63
XX 1 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKGKTN----- 51
XX
XX 64 LIISLAVFLMFLRLKISSEPLKDFKNTGSG-----LLGMANIDLEKSRGTG 110
XX 52 -----GGGGDKTHTCPPCPAPELGGPSVFLFPPKPK 84
XX
XX 111 DEILPRGLETVBECTEDCIKSKPKVDS-----HCFPLPAMEE-----GATIL 156
XX 85 DTLMSIRTPETV---CVVVDVSHEDPEVKFNWYDVGVEVHNKTKPREEQYNSTYRVVSV 141
XX 157 VTTKNDY-----CKSLPALSALETEKSIS 182
XX 142 LTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 173
XX
XX RESULT 30
XX AAE15485
```

AAE15485 standard; peptide; 51 AA.
AAE15485;
12-MAR-2002 (first entry)
Human B-cell maturation (BCMA) protein extracellular domain.
Human; transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
Homo sapiens.
WO200187979-A2.
22-NOV-2001.
14-MAY-2001; 2001WO-US015567.
12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
(AMGE-) AMGEN INC.
Theill LE, Yu G;
WPI; 2002-066686/09.
Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand.
Claim 1; Fig 10A; 94pp; English.
The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein extracellular domain
Sequence 51 AA;
Query Match 29.5%; Score 284; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 MAGCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGNTA 54
Dy 1 MAGCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKGNTA 51

RESULT 31
AAE15486
ID AAE15486 standard; peptide; 34 AA.
XX
XX
AC AAE15486;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
XX
PR 27-JUN-2000; 2000US-0214591P.
XX
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theill LE, Yu G;
XX
PI WPI; 2002-066686/09.
XX
DR Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
PS Claim 1; Fig 10A; 94pp; English.
XX
PS The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA protein extracellular domain
XX
SQ Sequence 34 AA;
Query Match 20.9%; Score 201; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 41
Dy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORYC 34

RESULT 32
 ID ADA49366 standard; peptide, 34 AA.
 XX
 AC ADA49366;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human BCMA cysteine rich domain.
 XX
 KW TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;
 KW antiarthritic; dermatological; antidiabetic; neuroprotective;
 KW antithyroid; antipyrretic; nephrotropic; vasotropic; vaccine;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW insulin dependent diabetes mellitus; multiple sclerosis;
 KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
 KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
 KW pemphigus vulgaris; acute rheumatic fever;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
 KW cysteine rich domain.
 XX
 OS Homo sapiens.
 XX
 OS WO2003035846-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 24-OCT-2002; 2002WO-US034376.
 XX
 PF 24-OCT-2001; 2001US-0345106P.
 XX
 PR 14-JAN-2002; 2002US-0348962P.
 XX
 PR 07-FEB-2002; 2002US-0354966P.
 XX
 PR 13-AUG-2002; 2002US-0403364P.
 XX
 XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI Zhang G, Shu H, Liu Y, Xu L;
 XX
 DR WPI; 2003-403345/38.
 XX
 XX Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological
 PT activity in mammal, has a modification in the region connecting beta
 PT strands D and E that reduces the biological activity of TALL-1
 PT antagonist.
 XX
 PS Disclosure; Page 616; 618pp; English.
 XX
 CC The invention relates to a novel TALL-1 antagonist protein, comprising a
 CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
 CC NO:2, by at least one modification in the region connecting E&G; strands
 CC D and E that reduces the biological activity of the TALL-1 antagonist as
 CC compared to wild-type TALL-1. A protein of the invention has
 CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyrretic,
 CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
 CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
 CC biological activity in a mammal. TC is useful for treating autoimmune
 CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
 CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
 CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
 CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and
 CC polyarteritis nodosa. The present sequence represents a cysteine rich
 CC domain (CRD) module of human BCMA.
 XX
 SQ Sequence 34 AA;
 Query Match 20.9%; Score 201; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.7e-14;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41
 |||||
 Db 1 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
 |||||
 RESULT 33
 ID AAE15489 standard; protein; 281 AA.
 XX
 AC AAE15489;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse BCMA-human immunoglobulin Fc region fusion protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 FN WO200187979-A2.
 XX
 XX 22-NOV-2001.
 PD
 XX 14-MAY-2001; 2001WO-US015567.
 XX
 PR 12-MAY-2000; 2000US-0204039P.
 PR 27-JUN-2000; 2000US-0214591P.
 PR 14-MAY-2001; 2001US-00214591.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Theill LE, Yu G;
 XX
 DR WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family
 PT ligand.
 XX
 PS Disclosure; Fig 10B; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.
 CC (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 281 AA;

Query Match 19.4%; Score 187; DB 5; Length 281;
Best Local Similarity 29.8%; Pred. No. 2.9e-11;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;

QY 4 MAGQCSQNEYPDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTAAILWTCLGLS 63
DB 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCPQYDPSVTSSVKGSS----- 47

QY 64 LIISLAVFLMFLRLKISSEPLKDFKNTGSG-----LLGMANIDLEKSR 108
DB 48 -----YTGCGGDKTKTCPCPAPELGGPSVFLPPK 80

QY 109 TGDRIILPRGLETVBECTCDECIKSPKVDSD-----HCFPLPAMEE-----GAT 154
DB 81 PKDTLMISRTPEVT--CVVDVSHEDPEVKFNWVDGVEVHNAKTKPREQYNSTYRVV 137

QY 155 ILVTTKTNDY-----CKSLPAALSATEIEKSSIS 182
DB 138 SVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 171

RESULT 34
ABJ38417

ID ABJ38417 standard; protein; 42 AA.

XX AC ABJ38417;

XX DT 12-JUN-2003 (first entry)

XX DE TALL-1 related protein SEQ ID No 197.

XX KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
KW gene therapy.

XX OS Homo sapiens.

XX PN W0200292620-A2.

XX PD 21-NOV-2002.

XX PF 13-MAY-2002; 2002WO-US015273.

XX PR 11-MAY-2001; 2001US-0290196P.

XX PA (AMGE-) AMGEN INC.

XX PI Min H, Hsu H;

XX DR WPI; 2003-156719/15.

XX PT New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas.

XX PS Disclosure; Page 26; 236pp; English.

XX CC The invention relates to a novel TALL-1-binding polypeptide comprising a
CC defined sequence in the specification. The composition is useful in
CC modulating the activity of TALL-1, and in treating, preventing,
CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer
CC lymphoma. The composition may also be used in treating inflammations
CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis

CC and vasculitis. Disorders may be treated with the novel composition using
CC gene therapy. This sequence represents a TALL-1 related protein of the
CC invention

XX SQ Sequence 42 AA;

Query Match 16.4%; Score 158; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQWAGQCSQNEYPDSLHACIPQLRCC 28
DB 15 MLQWAGQCSQNEYPDSLHACIPQLRCC 42

RESULT 35
ADI53060

ID ADI53060 standard; peptide; 26 AA.

XX AC ADI53060;

XX DT 22-APR-2004 (first entry)

XX DE Human BCVA receptor binding site.

XX KW protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;
KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW antidiabetic; dermatological; antiasthmatic; neurokine-alpha;
KW crystallography; cancer; allergic disorder; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
KW systemic lupus erythematosus; asthma; receptor.

XX OS Homo sapiens.

XX PN W02003050134-A2.

XX PD 19-JUN-2003.

XX PF 07-NOV-2002; 2002WO-US035561.

XX PR 07-NOV-2001; 2001US-0331049P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Oren DE, Arnold E, Volovik Y;

XX DR WPI; 2003-532895/50.

XX PT New crystalline Neutrokin-alpha protein, useful for designing compounds
PT that bind, inhibit or mimic a Neutrokin-alpha protein or enhance the
PT activity of a Neutrokin-alpha protein for treating e.g. cancer or
PT allergic disorders.

XX PS Disclosure; Fig 4; 362pp; English.

XX CC The invention relates to a neutrokin-alpha protein in crystalline form.
CC The crystalline neutrokin-alpha protein is useful for designing
CC molecules that have biological activity or compounds that bind, inhibit
CC or mimic a neutrokin-alpha protein and/or enhance the activity of a
CC neutrokin-alpha protein. The three-dimensional structure of a neutrokin
CC -alpha protein is useful in determining the three-dimensional of other
CC neutrokin-alpha proteins and their homologs. The compounds that mimic,
CC prevent or inhibit the activity of the protein are useful for treating
CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
CC erythematosus or asthma. This sequence represents the residues in the
CC receptor for binding a cytokine ligand.

XX SQ Sequence 26 AA;

Query Match 15.7%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 12 EYFDSLLHACIPQCLRCSSNTPLTLC 37
DB 1 EYFDSLLHACIPQCLRCSSNTPLTLC 26

RESULT 36
ABB78398
ID ABB78398 standard; protein; 175 AA.
XX
AC ABB78398;
XX
DT 17-DEC-2002 (first entry)
XX
DE Amino acid sequence of murine TRAF3-binding B cell-specific receptor.
XX
KW Mouse; TRAF3-binding B cell-specific receptor; TRAF3;
KW signal transduction; TNF ligand; cancer; autoimmune disease; apoplexia;
KW viral infection; AIDS; bone disease; transplantation rejection;
KW Alzheimer's disease; ischaemia; rheumatoid arthritis; cachexia.
XX
OS Mus sp.
XX
XX WO200272827-A1.
XX
PD 19-SEP-2002.
XX
PF 28-FEB-2002; 2002WO-JP001849.
XX
PR 28-FEB-2001; 2001JP-00055119.
XX
PA (RIKE ) RIKEN KK.
PA (IRIE/) IRIE S.
PA (SATO/) SATO T.
XX
PI Irie S, Sato T;
XX
XX WPI; 2002-713516/77.
XX
DR N-PSDB; ABV72373.
XX
XX TRAF3-binding B cell-specific receptor and encoded gene, applicable in
XX diagnosis of abnormality due to TRAF3-mediated intracellular signal
XX transduction and in screening drugs for e.g. cancer, autoimmune diseases
XX and AIDS.
XX
PS Claim 1; Page 47-48; 57pp; Japanese.
XX
CC The present sequence represents a murine TRAF3-binding B cell-specific
CC receptor. The polynucleotide and polypeptide sequence of this receptor
CC are useful for diagnosis of abnormality due to TRAF3-mediated
CC intracellular signal transduction and in screening drugs for diseases
CC associated with TNF ligand family and TNF receptor-ligand superfamily
CC e.g. cancer, autoimmune diseases, viral infections like AIDS, bone
CC diseases, transplantation rejection, Alzheimer's disease, ischaemia,
CC rheumatoid arthritis, apoplexia and cachexia
XX
SQ Sequence 175 AA;
Query Match 12.1%; Score 116.5; DB 5; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.00056;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 7 QCSQNEVFDSLLHACIPQCL-----RCSNTPLTLCQRYCNASVTVNSVK---GTNAIL 56
DB 21 QCNQTECFDPLVRNCVSCSELFTPTDGTHTSSLEPGTALQPOEGSALRPDVALLVGAPALL 80
QY 57 WTCGLSLI--ISLAVFMPLLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSTGD 111
DB 81 GLILALTLVGLVSLVSWRQQLRTASPDTSSEGVQOE-----SLENVFPVSSET-- 129
QY 112 BILIPRGLEYTVECTCEDCKIKSPKVDSDHCFPLPAMEGATILVTTKT 161
DB 130 ----PHASAPTWPLK-EDADSAUPR-----HSVPVPATELGSLTELVTIKT 170

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us-10-077-137-1.rag

RESULT 37

AAE22244

ID AAE22244 standard; protein; 175 AA.

XX

AC AAE22244;

XX

DT 25-JUL-2002 (first entry)

XX

DE Murine BAFF receptor (BAFF-R) protein.

XX

XX Murine; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation;

XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;

XX myasthenia gravis; hypertension; organ transplantation; drug screening;

XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular; TNF;

XX renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;

XX haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;

XX multiple myeloma; chromosomal mapping; tissue typing; drug screening.

XX

OS Mus musculus.

XX

XX Key Location/Qualifiers

XX Domain 70..97

XX /label= Transmembrane_domain

XX

XX WO200224909-A2.

XX

PD 28-MAR-2002.

XX

XX 06-SEP-2001; 2001WO-US028006.

XX

XX 18-SEP-2000; 2000US-0233152P.

XX

XX 21-SEP-2000; 2000US-0234140P.

XX

XX 13-FEB-2001; 2001US-0268499P.

XX

XX 14-AUG-2001; 2001US-0312185P.

XX

XX (BIOJ) BIOGEN INC.

XX

XX Ambrose CM, Thompson JS;

XX

XX WPI; 2002-362428/39.

XX

XX N-PSDB; AAD35411.

XX

XX New human BAFF receptor proteins and nucleic acids, useful for treating,

XX preventing or delaying e.g. autoimmune diseases, cancers, inherited

XX genetic disorders involving B-cells, cardiovascular disorders, or renal

XX disorders.

XX

XX Example 4; Fig 4b; 164pp; English.

XX

XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and

XX proteins. BAFF-R is a B-cell activating factor belonging to the Tumour

XX Necrosis Factor (TNF) family, which is associated with the expression of

XX B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are

XX useful for treating, preventing or delaying autoimmune diseases, cancer,

XX tumorigenic conditions or inherited genetic disorders involving B-cells,

XX hypertension, cardiovascular disorders, immunosuppressive diseases, renal

XX disorders, inflammation, organ transplantation and HIV. Autoimmune

XX diseases, which can be treated or prevented by BAFF-R, include systemic

XX lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune

XX haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease

XX Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,

XX poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma

XX cells disorders e.g., multiple myeloma, Waldenström's macroglobulinaemia,

XX heavy-chain disease, primary or immunocyte-associated amyloidosis, and

XX monoclonal gammopathy of undetermined significance. The nucleic acids,

XX protein, protein homologues, and antibodies may further be used in

XX screening assays, in detection assays (chromosomal mapping, tissue typing

XX or forensic biology), predictive medicine (e.g. diagnostic or prognostic

XX assays, monitoring clinical trials, or pharmacogenomic). The polypeptides

XX are further useful as immunogens to raise anti-BAFF-R antibodies, or in

XX screening drugs or compounds that modulate BAFF-R activity or expression.

XX The present sequence represents a murine BR3 polypeptide. The
CC specification also describes TAC1 polypeptides. TAC1 and BR3 are
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to
CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for
CC preparing a composition for treating systemic lupus erythematosus
XX
SQ Sequence 175 AA;

Query Match 12.1%; Score 116.5; DB 6; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.00056;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

Qy 7 QCSNEYFDSLHACIPCOL-----RCSNTPLTCQRYCNASVNSVK---GTNAIL 56
Db 21 QCNTECFDPLVRNCVSCLEFHTDTHGTSLEFGTALQPEGSAIPDVALVGPALL 80

Qy 57 WTCIGLSLI--ISLAVFLMFLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTD 111
Db 81 GLILALTLVGLVSLVSWRQRLRTASPDTSQGVQOE-----SLENVFPVPSSET-- 129

Qy 112 EIILPRGLETVVECTCEDCKSKPKVDSHCFPLPAMEEGATILVTTKT 161
Db 130 ----PHASAPTPPLK-EDADSALPR----HSVPVPATELGSGTELVTTKT 170

RESULT 40
AAE22266
ID AAE22266 standard; protein; 185 AA.
XX
AC AAE22266;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P.
XX
KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
KW myasthenia gravis; hypertension; organ transplantation; drug screening;
KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
FT Misc-difference 27 /note= "Wild type Leu substituted with Pro"
XX
FN WO200224909-A2.
XX
PD 28-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-US028006.
XX
PR 18-SEP-2000; 2000US-0233152P.
PR 21-SEP-2000; 2000US-0234140P.
PR 13-FEB-2001; 2001US-0268499P.
PR 14-AUG-2001; 2001US-0312185P.
XX
PA (BIOJ) BIOGEN INC.
XX
XX Ambrose CM, Thompson JS;
XX

DR WPI; 2002-362428/39.
XX
XX New human BAFF receptor proteins and nucleic acids, useful for treating,
PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
PT genetic disorders involving B-cells, cardiovascular disorders, or renal
PT disorders.
XX
PS Example 17; Page; 164pp; English.
XX
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BFR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant. Note: The present
CC sequence is not shown in the specification but is derived from human BAFF
CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
CC specification
XX
SQ Sequence 185 AA;

Query Match 11.0%; Score 106.5; DB 5; Length 185;
Best Local Similarity 26.4%; Pred. No. 0.0071;
Matches 48; Conservative 23; Mismatches 62; Indels 49; Gaps 8;

Qy 8 CSNEYPSDLHACIPCOL-----RCSNTPLTC---QRYCNASVNSVKGNAL 55
Db 19 CNOTECFDPLVRNCVACGLLTPRKPAGASSPAPRTALQPQESVGAGAGAAALPLPGL 78

Qy 56 LW---TCIGLSLIISLAVFLMF-----LLRKTSEPLKDFKNTGSGLLGMANIDLEK 106
Db 79 LFGAPALLGLVALLVGLVSWRRLRQRRLRGASSAEAPDGKDAPEPL----- 128

Qy 107 SRTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTT 159
Db 129 ----DKVII---LSPGISDATAWPPPGDPGTPP-----GHSVPVPATELGSGTELVT 177

Qy 160 KT 161
Db 178 KT 179

RESULT 41
AAE22267
ID AAE22267 standard; protein; 185 AA.
XX
XX AAE22267;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T.
XX
XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
XX myasthenia gravis; hypertension; organ transplantation; drug screening;
XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
XX

KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
mutant; mutein.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"
FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
XX

XX WO200224909-A2.
XX 28-MAR-2002.
XX 06-SEP-2001; 2001WO-US028006.
XX 18-SEP-2000; 2000US-0233152P.
XX 21-SEP-2000; 2000US-0234140P.
XX 13-FEB-2001; 2001US-0268499P.
XX 14-AUG-2001; 2001US-0312185P.
XX

XX (SIOJ) BIOGEN INC.
XX Ambrose CM, Thompson JS;
XX WPI; 2002-362428/39.
XX New human BAFF receptor proteins and nucleic acids, useful for treating,
PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
PT genetic disorders involving B-cells, cardiovascular disorders, or renal
PT disorders.
XX

XX Example 17; Page; 164pp; English.
XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
CC Necrosis Factor (TNF) family, which is associated with the expression of
CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
CC useful for treating, preventing or delaying autoimmune diseases, cancer,
CC tumorigenic conditions or inherited genetic disorders involving B-cells,
CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
CC disorders, inflammation, organ transplantation and HIV. Autoimmune
CC diseases, which can be treated or prevented by BAFF-R, include systemic
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
CC monoclonal gammopathy of undetermined significance. The nucleic acids,
CC protein, protein homologues, and antibodies may further be used in
CC screening assays, in detection assays (chromosomal mapping, tissue typing
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
CC are further useful as immunogens to raise anti-BFR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant. Note: The present
CC sequence is not shown in the specification but is derived from human BAFF
CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
CC specification
XX

XX SQ Sequence 185 AA;
Query Match 10.9%; Score 105.5; DB 5; Length 185;
Best Local Similarity 26.4%; Pred. No. 0.0091;
Matches 48; Conservative 23; Mismatches 62; Indels 49; Gaps 8;

Qy 8 CSQNEYFDSLHACIPQCL-----RCSNTPPLTC---QRNCNASVTNSVKGTNAI 55

Db 19 CNOTECFDLLRVHCVAGCLRTPRPKPAGAASSPAPRTALQPSVSGAGAEALPLPGL 78
Qy 56 LW---TCGLSLIISLAVFVLMF-----LLRKISSEPLKDEPKNTGSLGLGMANIDLEK 106
Db 79 LFGAPALLGLALVALVGLVSRRRQRRLRGASSAAEPDGKDAPEPL----- 128
Qy 107 SRTGDEIILPRGLEVTVECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTT 159
Db 129 ----DKVII---LSPGISDATAPAWPPGSDPGTTP-----GHSVPVPATELGSTELVTT 177
Qy 160 KT 161
Db 178 KT 179

RESULT 42
AAE15487
ID AAE15487 standard; peptide; 21 AA.
XX
AC AAE15487;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein transmembrane region.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.

XX WO200187979-A2.
XX 22-NOV-2001.
XX 14-MAY-2001; 2001WO-US015567.
XX 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
XX 14-MAY-2001; 2001US-00214591.
XX (AMGE-) AMGEN INC.
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.

XX Disclosure; Fig 10A; 94pp; English.
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering a
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung

CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein transmembrane region

XX Sequence 21 AA;

Query Match 10.8%; Score 104; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00075; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

QY 55 ILWTCGLSLIISLAVFLVLMF 75
 Db 1 ILWTCGLSLIISLAVFLVLMF 21

RESULT 43

AAE22269
 ID AAE22269 standard; protein; 185 AA.

XX AAE22269;

XX 25-JUL-2002 (first entry)

DE Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.

XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 KW mutant; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 20 /note= "Wild type Val substituted with Asn"

FT Misc-difference 21 /note= "Wild type Pro substituted with Gln"

XX WO200224909-A2.

XX 28-MAR-2002.

XX 06-SEP-2001; 2001WO-US028006.

XX 18-SEP-2000; 2000US-0233152P.

XX 21-SEP-2000; 2000US-0234140P.

XX 13-FEB-2001; 2001US-0268499P.

XX 14-AUG-2001; 2001US-0312185P.

XX (BIOJ) BIOGEN INC.

XX Ambrose CM, Thompson JS;

XX WPI; 2002-362428/39.

XX New human BAFF receptor proteins and nucleic acids, useful for treating,
 PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
 PT genetic disorders involving B-cells, cardiovascular disorders, or renal
 PT disorders.

XX Example 17; Page; 164pp; English.

XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are.

CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma. Waldenström's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BaFF-R antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant. Note: The present
 CC sequence is not shown in the specification but is derived from human BAFF
 CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
 CC specification

XX Sequence 185 AA;

Query Match 10.7%; Score 103.5; DB 5; Length 185;
 Best Local Similarity 26.4%; Pred. No. 0.015;
 Matches 48; Conservative 23; Mismatches 62; Indels 49; Gaps 8;

QY 8 CSQNEYPDSLHLHACIPQL-----RCSSTPPLTC---QRYCNASTVNSVKGNAI 55
 Db 19 CNOAECFDLVRHCACGLLRTPPKPAGAASSPAPRTALQPQESVGAGAGEAALPLPGL 78

QY 56 LW---TCGLSLIISLAVFLVLMF-----LLRKTSSEPLKDEPKNTSGSLGMANIDLEK 106

Db 79 LFGAPALLGLALVLVLVGLVSWRRRQRRLRGASSAEPDGKDAPEP----- 128

QY 107 SRTGDEIILPRGLETVVEECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTT 159

Db 129 -----DKVII---LSPGISDATAWPPPGEDPGTTP-----GHSVPVPATELGSELVTT 177

QY 160 KT 161

Db 178 KT 179

RESULT 44

AAE22271
 ID AAE22271 standard; protein; 185 AA.

XX AAE22271;

XX 25-JUL-2002 (first entry)

XX Human BAFF receptor (BAFF-R) mutant, P21Q.

XX Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
 KW Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
 KW myasthenia gravis; hypertension; organ transplantation; drug screening;
 KW HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
 KW renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
 KW haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
 KW multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 KW mutant; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 21

FT /note= "Wild type Pro substituted with Gln"

XX WO200224909-A2.

PD 28-MAR-2002.
 XX
 XX
 XX 06-SEP-2001; 2001WO-US280006.
 XX
 XX
 XX 18-SEP-2000; 2000US-0233152P.
 PR 21-SEP-2000; 2000US-0234140P.
 PR 13-SEP-2001; 2001US-0268499P.
 PR 14-AUG-2001; 2001US-0312185P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 XX Ambrose CM, Thompson JS;
 XX
 XX WPI; 2002-362428/39.
 XX
 XX New human BAFF receptor proteins and nucleic acids, useful for treating,
 PT preventing or delaying e.g. autoimmune diseases, cancers, inherited
 PT genetic disorders involving B-cells, cardiovascular disorders, or renal
 PT disorders.
 XX
 XX
 PS Example 17; Page; 164pp; English.
 XX
 XX The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
 CC proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
 CC Necrosis Factor (TNF) family, which is associated with the expression of
 CC B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
 CC useful for treating, preventing or delaying autoimmune diseases, cancer,
 CC tumorigenic conditions or inherited genetic disorders involving B-cells,
 CC hypertension, cardiovascular disorders, immunosuppressive diseases, renal
 CC disorders, inflammation, organ transplantation and HIV. Autoimmune
 CC diseases, which can be treated or prevented by BAFF-R, include systemic
 CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
 CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
 CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
 CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
 CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
 CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and
 CC monoclonal gammopathy of undetermined significance. The nucleic acids,
 CC protein, protein homologues, and antibodies may further be used in
 CC screening assays, in detection assays (chromosomal mapping, tissue typing
 CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
 CC are further useful as immunogens to raise anti-BAFF-R antibodies, or in
 CC screening drugs or compounds that modulate BAFF-R activity or expression.
 CC The present sequence is human BAFF-R protein mutant. Note: The present
 CC sequence is not shown in the specification but is derived from human BAFF
 CC -R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
 CC specification
 XX
 XX SQ Sequence 185 AA;
 Query Match 10.4%; Score 100.5; DB 5; Length 185;
 Best Local Similarity 26.4%; Pred. No. 0.031;
 Matches 48; Conservative 22; Mismatches 63; Indels 49; Gaps 8;
 QY 8 CSQNEYFDLSLHACIPCOL-----RCSNTPPLTC---QRVCNASVTNSVKGTNAI 55
 DB 19 CVQAECDLLVRHCVCGLLTPRPKAGASSPAPRTALQPQSVGAGAAALPUGL 78
 QY 56 LW-----TCGLSLIISLAVFLVLF-----LRKISSEPLKDFKNTGSGLLGHMANIDLE 106
 DB 79 LFGAPALLGLALVIALVLGLVSVRRQRRLRGASSAEAPDGDKDAPEPL-----128
 QY 107 SRTGDEIILPRGLEVTVEECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTT 159
 DB 129 -----DKVII---LSFGISDATAPAWPPPGEDGTTP-----GHSVPVPTELSTELVTT 177
 QY 160 KT 161
 DB 178 KT 179
 RESULT 45

ADB90663
 ID ADB90663 standard; protein; 185 AA.
 XX
 XX ADB90663;
 AC
 XX
 XX 04-DEC-2003 (first entry)
 DT
 XX
 XX TALL-IR gene.
 DE
 XX
 XX Antirheumatic; tumor necrosis factor; apoptosis; TALL-IR;
 KW rheumatoid arthritis; systemic lupus erythematosus; B cell neoplasm;
 KW multiple myeloma; immune function; Antiarthritic; Immunosuppressive;
 KW Dermatological; Antiinflammatory; Fungicide; Protozoacide; Antibacterial;
 KW Virucide; Antidiarrhetic; Antipsoriatic; Antiallergic; Antiaesthetic;
 KW Neuroprotective; Antidiabetic; Cytostatic.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003024991-A2.
 PN
 XX
 XX 27-MAR-2003.
 PD
 XX
 XX 20-SEP-2002; 2002WO-US030009.
 PF
 XX
 XX 21-SEP-2001; 2001US-0324238P.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Hau H;
 PI
 XX
 XX WPI; 2003-421121/39.
 DR
 XX
 XX N-PSDB; ADB90662.
 DR
 XX
 XX Novel tumor necrosis factor and apoptosis ligand-related leukocyte-
 PT expressed ligand 1 receptor polypeptide, useful for treating rheumatoid
 PT arthritis, systemic lupus erythematosus, B cell neoplasm, or multiple
 PT myeloma.
 PT
 XX
 XX Claim 1; Page 122; 130pp; English.
 PS
 XX
 XX The present invention relates to a tumor necrosis factor and apoptosis
 CC ligand-related leukocyte-expressed ligand 1 receptor (TALL-IR)
 CC polypeptide. The polypeptide of the invention is useful for treating,
 CC preventing, or ameliorating a medical disease, condition or disorder,
 CC preferably a TALL-IR polypeptide-related disease, where the disease
 CC condition or disorder is rheumatoid arthritis, systemic lupus
 CC erythematosus, a B cell neoplasm, multiple myeloma, or is associated with
 CC inflammation or immune function. The polypeptide is useful for diagnosing
 CC a pathological condition or a susceptibility to a pathological condition
 CC in a subject. The present sequence represents a TALL-IR gene of the
 CC invention.
 XX
 XX SQ Sequence 185 AA;
 Query Match 10.4%; Score 100; DB 7; Length 185;
 Best Local Similarity 23.8%; Pred. No. 0.035;
 Matches 44; Conservative 25; Mismatches 62; Indels 54; Gaps 8;
 QY 8 CSQNEYFDLSLHACIPCOLRCSNTPPLTCQRVCNASVTNSVKGT-----52
 DB 19 CVPTCYDILLVRKVCVCRLLRKS--PKTA-----AGASSPAPGTALQPQSVGTGSGEV 71
 QY 53 ----NAILW---TCGLSLIISLAVFLVLFMLLRKISSEPLKDFKNTGSGLLGHMANIDLE 105
 DB 72 SLPLPGLLFCAPALLGLVVLVVLVGLV-----SWRRRQRLRGNASTE-- 116
 QY 106 KSRTGDEIILPRGLEVTYV--EECTCEDCIKSKPKVDS-----HCFPLPAMEEGATIL 156
 DB 117 -APDGDKAAPPEPLDKVILSPGTDTATAPWPPPGEDQGTTPPGHSHIPVATELGSTEL 175
 QY 157 VTTKT 161
 DB 176 VTTKT 180

```
CC are further useful as immunogens to raise anti-BFRR antibodies, or in
CC screening drugs or compounds that modulate BAFF-R activity or expression.
CC The present sequence is human BAFF-R protein mutant. Note: The present
CC sequence is not shown in the specification but is derived from human BAFF
CC -R referred as SEQ ID NO: 5 (AAE222242) and shown in fig 2d of the
CC specification
XX
XX SQ Sequence 185 AA;

Query Match 10.3%; Score 99.5; DB 5; Length 185;
Best Local Similarity 25.8%; Pred.No. 0.04; Mismatches 23; Indels 49; Gaps 8;
Matches 47; Conservative 23;

Qy 8 CSQNEYDLSLHACIPCOL-----RCSNTPTLC---QRYCNASVTSNYSVGTNAI 55
Db 19 CNPTECFDLVRHCVACGLLRTPRPKAGAAASPAPRTALQPQESVGAGAGEAALPLPGL 78
Qy 56 LW---TCIGUSLILSLAVFVMP-----LRRKISSEPLKDEPKNTGSGLLGMANIDLEK 106
Db 79 LFGAPALLGLALVLLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL----- 128
Qy 107 SRTGDEIILPRGLETVVEECTC-----EDCIKSKPKVSDHCFPLPAMEEGATILVTT 159
Db 129 ----DKVII---LSPGISDATAPANPPPGSDPGTTPP-----GHSVPVFATELGSTELVTT 177
Qy 160 KT 161
Db 178 KT 179

RESULT 47
AAE22270
ID AAE22270 standard; protein; 185 AA.
XX
XX AC AAE22270;
XX
XX DT 25-JUL-2002 (first entry)
XX
XX DE Human BAFF receptor (BAFF-R) mutant, V20N.
XX
XX KW Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;
XX myasthenia gravis; hypertension; organ transplantation; drug screening;
XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
XX renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;
XX haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;
XX multiple myeloma; chromosomal mapping; tissue typing; drug screening;
XX mutant; mutein.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 20 /note= "Wild type Val substituted with Asn"
XX FT Misc-difference 22 /note= "Wild type Ala substituted with Thr"
XX
XX WO200224909-A2.
XX
XX PD 28-MAR-2002.
XX
XX PF 06-SEP-2001; 2001WO-US028006.
XX
XX PR 18-SEP-2000; 2000US-0233152P.
XX PR 21-SEP-2000; 2000US-0234140P.
XX PR 13-FEB-2001; 2001US-0268499P.
XX PR 14-AUG-2001; 2001US-0312185P.
XX
XX PA (BIOJ ) BIOGEN INC.
XX
XX PI Ambrose CM, Thompson JS;
XX
XX DR WPI; 2002-362428/39.
XX
XX PT New human BAFF receptor proteins and nucleic acids, useful for treating,
XX preventing or delaying e.g. autoimmune diseases, cancers, inherited
XX genetic disorders involving B-cells, cardiovascular disorders, or renal
XX disorders.
XX
XX PS Example 17; Page; 164pp; English.
XX
XX CC The invention relates to human BAFF receptor (BAFF-R) nucleic acids and
XX proteins. BAFF-R is a B-cell activating factor belonging to the Tumour
XX Necrosis Factor (TNF) family, which is associated with the expression of
XX B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
XX useful for treating, preventing or delaying autoimmune diseases, cancer,
XX tumorigenic conditions or inherited genetic disorders involving B-cells,
XX hypertension, cardiovascular disorders, immunosuppressive diseases, renal
XX disorders, inflammation, organ transplantation and HIV. Autoimmune
XX diseases, which can be treated or prevented by BAFF-R, include systemic
XX lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune
XX haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease
XX Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,
XX poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma
XX cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,
XX heavy-chain disease, primary or immunocyte-associated amyloidosis, and
XX monoclonal gammopathy of undetermined significance. The nucleic acids,
XX protein, protein homologues, and antibodies may further be used in
XX screening assays, in detection assays (chromosomal mapping, tissue typing
XX or forensic biology), predictive medicine (e.g. diagnostic or prognostic
XX assays, monitoring clinical trials, or pharmacogenomic). The polypeptides
```


Db 19 CVPACFDLLVRHCVACGLLTPRPKPAGASSAPARTALQPSVGVGAGAAALPLPGL 78
 Qy 56 LW---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
 Db 79 LFGAPALLGLALVLALVLGLVSWRRRRRLRGASSAEPDGDKAPEPL----- 128
 Qy 107 SRTGDEIILPRGLEVTVEECTC-----EDCIKSPKVDSDHCFPLPAMEEGATILVTT 159
 Db 129 ---DKVII---LSPGISDATAPAWPPGEDPGTTPP-----GHSVPVPATELGSSTELVTT 177
 Qy 160 KT 161
 Db 178 KT 179

RESULT 49

ABB81483
 ID ABB81483 standard; protein; 184 AA.

XX AC ABB81483;

XX DT 02-SEP-2002 (first entry)

XX XX Human Ztnfr12 protein SEQ ID NO:2.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasia; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypercension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease;
 KW chromosome 22q13.2.

XX OS Homo sapiens.

XX PN WO200238766-A2.

XX PD 16-MAY-2002.

XX PF 05-NOV-2001; 2001WO-US047018.

XX PR 07-NOV-2000; 2000US-0246449P.

XX PR 20-DEC-2000; 2000US-0257131P.

XX PR 28-JUN-2001; 2001US-0301715P.

XX PR 29-AUG-2001; 2001US-0315565P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX FI Gross JA, Xu W, Henne RM, Grant FJ;

XX DR WPI; 2002-508212/54.

XX DR N-PSDB; ABB89426.

XX PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
 PT renal failure or renal disease and lymphoma.

XX PS Claim 3; Page 133; 154pp; English.

XX CC The present sequence represents a human tumour necrosis factor receptor
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating

CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel disease. (I) is useful for
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. Human Ztnfr12 is located to chromosome 22q13.2

XX SQ Sequence 184 AA;

Query Match 9.6%; Score 93; DB 5; Length 184;

Best Local Similarity 26.5%; Pred. No. 0.2; Mismatches 65; Indels 48; Gaps 8;
 Matches 48; Conservative 20;

Qy 8 CSQNEVFDLSLHACIPCOL-----RCSSNTP--PLTCQRYCNASVNTSVKGTNAIL 56

Db 19 CVPACFDLLVRHCVACGLLTPRPKPAGASSAPARTALQPSVGVGAGAAALPLPGL 78

Qy 57 W---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS 107

Db 79 FGAPALLGLALVLALVLGLVSWRRRRRLRGASSAEPDGDKAPEPL----- 127

Qy 108 RTGDEIILPRGLEVTVEECTC-----EDCIKSPKVDSDHCFPLPAMEEGATILVTTK 160

Db 128 ---DKVII---LSPGISDATAPAWPPGEDPGTTPP-----GHSVPVPATELGSSTELVTTK 177

Qy 161 T 161

Db 178 T 178

RESULT 50

AAE35227
 ID AAE35227 standard; protein; 184 AA.

XX AC AAE35227;

XX DT 28-MAY-2003 (first entry)

XX DE Human Ztnfr12 receptor protein.

XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
 KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
 KW anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
 KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
 KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
 KW Ztnfr12; receptor.

XX OS Homo sapiens.

XX PN WO200294852-A2.

XX PD 28-NOV-2002.

XX PF 20-MAY-2002; 2002WO-US015910.

XX PR 24-MAY-2001; 2001US-0293343P.

XX XX (ZYMO) ZYMOGENETICS INC.

XX PI Rixon MW, Gross JA;

XX DR WPI; 2003-148455/14.

XX DR N-PSDB; AAD53776.

XX PT Transmembrane activator and calcium modulator and cyclophilin ligand-

PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.

diabetes, comprises a fast receptor group and an immunoglobulin group:

PS Disclosure; Col 136-137; 71pp; English.

YX

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100101102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200201202203204205206207208209210211212213214215216217218219220221222223224225226227228229230231232233234235236237238239240241242243244245246247248249250251252253254255256257258259260261262263264265266267268269270271272273274275276277278279280281282283284285286287288289290291292293294295296297298299300301302303304305306307308309310311312313314315316317318319320321322323324325326327328329330331332333334335336337338339340341342343344345346347348349350351352353354355356357358359360361362363364365366367368369370371372373374375376377378379380381382383384385386387388389390391392393394395396397398399400401402403404405406407408409410411412413414415416417418419420421422423424425426427428429430431432433434435436437438439440441442443444445446447448449450451452453454455456457458459460461462463464465466467468469470471472473474475476477478479480481482483484485486487488489490491492493494495496497498499500501502503504505506507508509510511512513514515516517518519520521522523524525526527528529530531532533534535536537538539540541542543544545546547548549550551552553554555556557558559560561562563564565566567568569570571572573574575576577578579580581582583584585586587588589590591592593594595596597598599600601602603604605606607608609610611612613614615616617618619620621622623624625626627628629630631632633634635636637638639640641642643644645646647648649650651652653654655656657658659660661662663664665666667668669670671672673674675676677678679680681682683684685686687688689690691692693694695696697698699700701702703704705706707708709710711712713714715716717718719720721722723724725726727728729730731732733734735736737738739740741742743744745746747748749750751752753754755756757758759760761762763764765766767768769770771772773774775776777778779780781782783784785786787788789790791792793794795796797798799800801802803804805806807808809810811812813814815816817818819820821822823824825826827828829830831832833834835836837838839840841842843844845846847848849850851852853854855856857858859860861862863864865866867868869870871872873874875876877878879880881882883884885886887888889890891892893894895896897898899900901902903904905906907908909910911912913914915916917918919920921922923924925926927928929930931932933934935936937938939940941942943944945946947948949950951952953954955956957958959960961962963964965966967968969970971972973974975976977978979980981982983984985986987988989990991992993994995996997998999100010011002100310041005100610071008100910101011101210131014101510161017101810191020102110221023102410251026102710281029103010311032103310341035103610371038103910401041104210431044104510461047104810491050105110521053105410551056105710581059106010611062106310641065106610671068106910701071107210731074107510761077107810791080108110821083108410851086108710881089109010911092109310941095109610971098109911001101110211031104110511061107110811091110111111121113111411151116111711181119112011211122112311241125112611271128112911301131113211331134113511361137113811391140114111421143114411451146114711481149115011511152115311541155115611571158115911601161116211631164116511661167116811691170117111721173117411751176117711781179118011811182118311841185118611871188118911901191119211931194119511961197119811991200120112021203120412051206120712081209121012111212121312141215121612171218121912201221122212231224122512261227122812291230123112321233123412351236123712381239124012411242124312441245124612471248124912501251125212531254125512561257125812591260126112621263126412651266126712681269127012711272127312741275127612771278127912801281128212831284128512861287128812891290129112921293129412951296129712981

Y

22 The invention relates to a system for

the invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human Ztnfr2 receptor protein

Sequence 184 AA;

Introduction

Query Match 9.6%; Score 93; DB 6; Length 184;

Best Local Similarity 26.5%; Pred. No. 0.2;

Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

QY 8 CSQNEYFDSLHACIPCQL-----RCSSNTP--PLTCORYCNASVTNSVKGTNAIL 56

19 CYPACFLLVRHCACGLLRTPRPKPAGASSPAPRTALPOBSVGAGAGEAALPLPGLL 78

QY 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS 107

db 79 FGAPALLGLALVLAALVTLVGLSVRRRQRRLRGASSAAEPDGDKDAPEPL----- 127

QY 108 RTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVSDHCFPLPAMEEGATILVTTK 160

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128 ---DKVII---LSPGISDATAPAWPPPPGDDPGTTPP-----GHSVVPVPA TELGSELVTTK 177
db

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Qy 161 T 161

—

Search completed: January 28, 2005, 19:52:41
Job time : 202.661 secs

Job time : 202.661 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:52:54 ; Search time 30.2569 Seconds
(without alignments)
405.985 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201

Sequence: 1 CSQNEYFDSLLHACIPQLRCSNTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 201 | 100.0 | 34 | 9 | US-09-854-864-7 |
| 2 | 201 | 100.0 | 34 | 9 | US-09-855-158-7 |
| 3 | 201 | 100.0 | 51 | 9 | US-09-854-864-6 |
| 4 | 201 | 100.0 | 51 | 9 | US-09-855-158-6 |
| 5 | 201 | 100.0 | 58 | 9 | US-09-854-864-21 |
| 6 | 201 | 100.0 | 58 | 9 | US-09-855-158-21 |
| 7 | 201 | 100.0 | 81 | 9 | US-09-854-864-13 |
| 8 | 201 | 100.0 | 81 | 9 | US-09-855-158-13 |
| 9 | 201 | 100.0 | 181 | 9 | US-09-854-864-5 |
| 10 | 201 | 100.0 | 181 | 9 | US-09-855-158-5 |
| 11 | 201 | 100.0 | 184 | 13 | US-10-077-438-1 |
| 12 | 201 | 100.0 | 184 | 13 | US-10-077-438-7 |
| 13 | 201 | 100.0 | 184 | 13 | US-10-077-137-1 |

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| 184 | 100.0 | 201 | 14 | 13 | US-10-077-137-7 | Sequence 7, Appli |
| 184 | 100.0 | 201 | 15 | 14 | US-10-068-725-2 | Sequence 2, Appli |
| 184 | 100.0 | 201 | 16 | 14 | US-10-151-882-47 | Sequence 47, Appli |
| 184 | 100.0 | 201 | 17 | 14 | US-10-115-192-8 | Sequence 8, Appli |
| 184 | 100.0 | 201 | 18 | 14 | US-10-115-192-8 | Sequence 7, Appli |
| 184 | 100.0 | 201 | 19 | 14 | US-10-152-363A-27 | Sequence 27, Appli |
| 184 | 100.0 | 201 | 20 | 14 | US-10-216-074-11 | Sequence 11, Appli |
| 184 | 100.0 | 201 | 21 | 14 | US-10-087-080-39 | Sequence 39, Appli |
| 184 | 100.0 | 201 | 22 | 17 | US-10-742-634-9 | Sequence 9, Appli |
| 283 | 100.0 | 201 | 23 | 9 | US-09-854-864-9 | Sequence 9, Appli |
| 283 | 100.0 | 201 | 24 | 9 | US-09-855-158-9 | Sequence 12, Appli |
| 302 | 100.0 | 201 | 25 | 14 | US-10-115-192-12 | Sequence 3, Appli |
| 207 | 90.0 | 181 | 26 | 13 | US-10-077-438-3 | Sequence 3, Appli |
| 207 | 90.0 | 181 | 27 | 13 | US-10-077-137-3 | Sequence 11, Appli |
| 185 | 67.7 | 136 | 28 | 9 | US-09-854-864-11 | Sequence 11, Appli |
| 185 | 67.7 | 136 | 29 | 9 | US-09-855-158-11 | Sequence 17, Appli |
| 185 | 67.7 | 136 | 30 | 14 | US-10-216-074-17 | Sequence 10, Appli |
| 281 | 67.7 | 136 | 31 | 9 | US-09-854-864-10 | Sequence 10, Appli |
| 281 | 67.7 | 136 | 32 | 9 | US-09-855-158-10 | Sequence 197, App |
| 42 | 61.7 | 124 | 33 | 14 | US-10-145-206-197 | Sequence 12, Appli |
| 117 | 46.5 | 93.5 | 34 | 9 | US-09-854-864-12 | Sequence 12, Appli |
| 117 | 46.5 | 93.5 | 35 | 9 | US-09-855-158-12 | Sequence 1647, Ap |
| 249 | 35.6 | 71.5 | 36 | 13 | US-10-087-192-1647 | Sequence 2, Appli |
| 37 | 67.5 | 66.5 | 37 | 9 | US-09-779-050A-45 | Sequence 45, Appli |
| 1548 | 33.1 | 66.5 | 38 | 9 | US-09-854-864-20 | Sequence 20, Appli |
| 37 | 67.5 | 66.5 | 39 | 9 | US-09-855-158-20 | Sequence 16, Appli |
| 59 | 33.1 | 66.5 | 40 | 9 | US-09-854-864-16 | Sequence 15, Appli |
| 67 | 33.1 | 66.5 | 41 | 9 | US-09-855-158-16 | Sequence 6, Appli |
| 67 | 33.1 | 66.5 | 42 | 9 | US-09-854-864-15 | Sequence 43, Appli |
| 166 | 33.1 | 66.5 | 43 | 9 | US-09-855-158-15 | Sequence 22, Appli |
| 166 | 33.1 | 66.5 | 44 | 14 | US-10-293-816-6 | Sequence 14, Appli |
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| 293 | 33.1 | 66.5 | 46 | 9 | US-09-879-919-22 | Sequence 42, Appli |
| 293 | 33.1 | 66.5 | 47 | 9 | US-09-854-864-14 | Sequence 1650, Ap |
| 293 | 33.1 | 66.5 | 48 | 9 | US-09-855-158-14 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 49 | 9 | US-09-361-376-2 | Sequence 4, Appli |
| 293 | 33.1 | 66.5 | 50 | 9 | US-09-779-050A-42 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 51 | 10 | US-09-302-863-2 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 52 | 10 | US-09-855-564-2 | Sequence 1650, Ap |
| 293 | 33.1 | 66.5 | 53 | 13 | US-10-087-192-1650 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 54 | 13 | US-10-084-971-2 | Sequence 4, Appli |
| 293 | 33.1 | 66.5 | 55 | 13 | US-10-068-725-4 | Sequence 46, Appli |
| 293 | 33.1 | 66.5 | 56 | 14 | US-10-151-882-46 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 57 | 14 | US-10-293-816-2 | Sequence 8, Appli |
| 293 | 33.1 | 66.5 | 58 | 14 | US-10-008-063-8 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 59 | 14 | US-10-152-363A-2 | Sequence 22, Appli |
| 293 | 33.1 | 66.5 | 60 | 14 | US-10-268-951-22 | Sequence 14, Appli |
| 293 | 33.1 | 66.5 | 61 | 14 | US-10-258-368-1 | Sequence 2, Appli |
| 293 | 33.1 | 66.5 | 62 | 15 | US-10-258-368-1 | Sequence 4, Appli |
| 293 | 33.1 | 66.5 | 63 | 15 | US-10-618-797-4 | Sequence 7, Appli |
| 293 | 33.1 | 66.5 | 64 | 17 | US-10-742-634-7 | Sequence 12, Appli |
| 293 | 33.1 | 66.5 | 65 | 17 | US-10-748-112-27 | Sequence 27, Appli |
| 301 | 33.1 | 66.5 | 66 | 15 | US-10-258-368-12 | Sequence 18, Appli |
| 301 | 33.1 | 66.5 | 67 | 14 | US-10-152-363A-62 | Sequence 62, Appli |
| 332 | 33.1 | 66.5 | 68 | 14 | US-10-258-368-8 | Sequence 8, Appli |
| 334 | 33.1 | 66.5 | 69 | 15 | US-10-152-363A-52 | Sequence 52, Appli |
| 344 | 33.1 | 66.5 | 70 | 14 | US-10-152-363A-54 | Sequence 54, Appli |
| 348 | 33.1 | 66.5 | 71 | 14 | US-10-152-363A-56 | Sequence 56, Appli |
| 357 | 33.1 | 66.5 | 72 | 15 | US-10-258-368-6 | Sequence 6, Appli |
| 366 | 33.1 | 66.5 | 73 | 14 | US-10-152-363A-50 | Sequence 50, Appli |
| 366 | 33.1 | 66.5 | 74 | 9 | US-09-854-864-18 | Sequence 18, Appli |
| 397 | 33.1 | 66.5 | 75 | 9 | US-09-855-158-18 | Sequence 15, Appli |
| 397 | 33.1 | 66.5 | 76 | 9 | US-10-258-368-15 | Sequence 75, Appli |
| 404 | 33.1 | 66.5 | 77 | 14 | US-10-028-248A-75 | Sequence 74, Appli |
| 5374 | 32.1 | 64.5 | 78 | 15 | US-10-107-782-75 | Sequence 251720, |
| 5374 | 32.1 | 64.5 | 79 | 14 | US-10-028-248A-74 | Sequence 337171, |
| 5376 | 32.1 | 64.5 | 80 | 15 | US-10-107-782-74 | Sequence 2, |
| 5376 | 32.1 | 64.5 | 81 | 15 | US-10-424-599-251720 | Sequence 21, Appli |
| 95 | 30.8 | 62 | 82 | 17 | US-10-425-115-337171 | Sequence 2804, Ap |
| 107 | 29.6 | 59.5 | 83 | 9 | US-09-886-429-2 | Sequence 10, Appli |
| 418 | 29.6 | 59.5 | 84 | 14 | US-10-162-435-21 | |
| 581 | 29.6 | 59.5 | 85 | 14 | US-10-104-047-2804 | |
| 735 | 29.6 | 59.5 | 86 | 9 | US-09-498-570-10 | |

87 59.5 29.6 735 10 US-09-839-446-10 Sequence 10, Appl
88 59.5 29.6 845 9 US-09-898-570-12 Sequence 12, Appl
89 59.5 29.6 845 10 US-09-839-446-12 Sequence 12, Appl
90 59.5 29.6 880 14 US-10-104-047-2834 Sequence 2834, Ap
91 59.5 29.6 897 14 US-10-239-663-35 Sequence 35, Appl
92 59.5 29.6 897 16 US-10-470-390A-12 Sequence 12, Appl
93 59.5 29.6 914 14 US-10-406-073-6 Sequence 6, Appl
94 59.5 29.6 939 16 US-10-480-172-22 Sequence 22, Appl
95 59.5 29.6 974 9 US-09-898-570-14 Sequence 14, Appl
96 59.5 29.6 974 10 US-09-839-446-14 Sequence 14, Appl
97 59.5 29.6 985 15 US-10-108-260A-2874 Sequence 2874, Ap
98 59.5 29.6 993 14 US-10-239-663-36 Sequence 36, Appl
99 59.5 29.6 993 14 US-10-406-073-8 Sequence 8, Appl
100 59.5 29.6 993 14 US-10-406-073-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-854-864-7
Query Match 100.0%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFDLSLLHACIPCOLRCSSNTPLTCQRYC 34
Db 1 CSQNEFDLSLLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 2
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match 100.0%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFDLSLLHACIPCOLRCSSNTPLTCQRYC 34
Db 1 CSQNEFDLSLLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 3
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-854-864-6
Query Match 100.0%; Score 201; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEFDLSLLHACIPCOLRCSSNTPLTCQRYC 34
Db 5 CSQNEFDLSLLHACIPCOLRCSSNTPLTCQRYC 38

RESULT 4
US-09-855-158-6
; Sequence 6, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-855-158-6
Query Match 100.0%; Score 201; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 38

RESULT 5

US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 100.0%; Score 201; DB 9; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 6

US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match 100.0%; Score 201; DB 9; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 7

US-09-854-864-13

; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match 100.0%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 8

US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match 100.0%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 9

US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-5

Query Match 100.0%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      100.0%; Score 201; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 38

RESULT 10
US-09-855-158-5
; Sequence 5, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5

Query Match      100.0%; Score 201; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 38

RESULT 11
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
US-10-077-438-1

Query Match      100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41

RESULT 12
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41

RESULT 13
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; FILE REFERENCE: A080PCT
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; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match      100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41

RESULT 12
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41

RESULT 13
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; FILE REFERENCE: A080PCT
```

APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 184
TYPE: PRT
ORGANISM: homo sapien
US-10-077-137-1

Query Match 100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 14

US-10-077-137-7
Sequence 7, Application US/10077137
Publication No. US20020172674A1
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 184
TYPE: PRT
ORGANISM: homo sapien
US-10-077-137-7

Query Match 100.0%; Score 201; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 15

US-10-068-725-2
Sequence 2, Application US/10068725
Publication No. US20030012783A1
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
FILE REFERENCE: 01-04
CURRENT APPLICATION NUMBER: US/10/068,725
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/270,274
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/283,447
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-068-725-2

Query Match 100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 16

US-10-151-882-47
Sequence 47, Application US/10151882
Publication No. US20030059862A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 47
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-151-882-47

Query Match 100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 34
DB 8 CSONEYFDSLHACIPCOLRCSNTPTLTQRYC 41

RESULT 17

US-10-115-192-8
Sequence 8, Application US/10115192
Publication No. US20030082175A1
GENERAL INFORMATION:
APPLICANT: Apotech R & D S.A.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REFERENCE: A083PCT
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02

```
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 18
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 19
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27
```

```
Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 20
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

RESULT 21
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorect
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
```

```
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match      100.0%; Score 201; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 22
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 201; DB 17; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 23
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match      100.0%; Score 201; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
```

```
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 38

RESULT 24
US-09-855-158-9
; Sequence 9, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match      100.0%; Score 201; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 5 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 38

RESULT 25
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match      100.0%; Score 201; DB 14; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db 31 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 64
```

RESULT 26

US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match 90.0%; Score 181; DB 13; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Qy 1 CSQNEYFDSL-----LHACIPQCLRCSSNTPTLTCMHACIPQCLRCSSNTPTLTCQRYC 34
| : |||||
Db 46 CSQNEYFDSLHACIPQCLRCSSNTPTLTCMHACIPQCLRCSSNTPTLTCQRYC 99

RESULT 27

US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3

Query Match 90.0%; Score 181; DB 13; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Qy 1 CSQNEYFDSL-----LHACIPQCLRCSSNTPTLTCQRYC 34
| : |||||
Db 46 CSQNEYFDSLHACIPQCLRCSSNTPTLTCMHACIPQCLRCSSNTPTLTCQRYC 99

RESULT 28

US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/Agp-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 67.7%; Score 136; DB 9; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.3e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQRYC 34
| : |||||
Db 5 CPHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 29

US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-855-158-11

Query Match 67.7%; Score 136; DB 9; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.3e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQRYC 34
| : |||||
| : |||||

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 30

US-10-216-074-17
; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: SHU, HONG-BING
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-074-17

Query Match 67.7%; Score 136; DB 14; Length 185;
Best Local Similarity 70.6%; Pred. No. 9.3e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 31

US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 67.7%; Score 136; DB 9; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 32

US-09-855-158-10
; Sequence 10, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match 67.7%; Score 136; DB 9; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 33

US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match 61.7%; Score 124; DB 14; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRRC 21

Db 22 CSQNEYFDSLHACIPQLRRC 42

RESULT 34

US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11

Query Match 33.1%; Score 66.5; DB 14; Length 166;
Best Local Similarity 32.4%; Pred. No. 2.4;
Matches 11; Conservative 8; Mismatches 14; Indels 1

Query Match 33.1%; Score 66.5; DB 14; Length 166;
Best Local Similarity 32.4%; Pred. No. 2.4;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDLLHACIPQLRCSSNTPLTCQRYC 34
 | : : | | | : : : : : : : : : :
Db 34 CPPEOYWDPLLGTCSCKTICNHOS-ORTCAAFc 66

```

RESULT 46
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TN
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/77
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

```

Query Match 33.1%; Score 66.5; DB 9; Length 291;
Best Local Similarity 32.4%; Pred. No. 4.2;
Matches 11: Conservative 8; Mismatches 14: Indels

| | | | |
|----|----|----------------------------------|----|
| Qy | 1 | CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC | 34 |
| | | : : : : : : : : | |
| Db | 34 | CPEQVDPPLLGTCMSCKTTCNHOS-ORTCAAF | 66 |

```

RESULT 47
US-09-879-919-22
/ Sequence 22, Application US/09879919
/ Patent No. US20020064829A1
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Guo-Liang, et al.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
/ FILE REFERENCE: PF253PI
/ CURRENT APPLICATION NUMBER: US/09/879,919
/ CURRENT FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,978
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/254,875
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 60/241,952
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/211,537
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 08/815,783
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: 60/016,812
/ PRIOR FILING DATE: 1996-03-14

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:45:08 ; Search time 40.5138 Seconds
(without alignments)
436.984 Million cell updates/sec

Title: US-10-077-137-1
Perfect score: 964
Sequence: 1 MLQWAGCQSQNEFDLSLHA.....CKSLPAALSATEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 964 | 100.0 | 184 | 2 S43486 | B-cell maturation |
| 2 | 88.5 | 9.2 | 217 | 2 C97344 | amino acid ABC tra |
| 3 | 86.5 | 9.0 | 858 | 2 T08891 | prominin - mouse |
| 4 | 83.5 | 8.7 | 1998 | 2 T13009 | protein-tyrosine k |
| 5 | 82 | 8.5 | 1009 | 2 A57434 | protein-tyrosine k |
| 6 | 81.5 | 8.5 | 2233 | 2 T28669 | surface protein 51 |
| 7 | 81 | 8.4 | 773 | 2 D89010 | protein R08F11.7 [|
| 8 | 79.5 | 8.2 | 1009 | 2 S60248 | protein-tyrosine k |
| 9 | 79.5 | 8.2 | 1299 | 2 T43251 | furin (EC 3.4.21.7 |
| 10 | 78.5 | 8.1 | 343 | 2 D64469 | potassium channel |
| 11 | 78 | 8.1 | 841 | 2 JC5894 | killer cell inhibi |
| 12 | 77.5 | 8.0 | 738 | 2 D86345 | hypothetical prote |
| 13 | 77.5 | 8.0 | 968 | 2 T01733 | hypothetical prote |
| 14 | 77 | 8.0 | 522 | 2 T45824 | hypothetical prote |
| 15 | 77 | 8.0 | 539 | 2 F72288 | methyl-accepting c |
| 16 | 76.5 | 7.9 | 357 | 2 T21552 | hypothetical prote |
| 17 | 76.5 | 7.9 | 1404 | 2 T19277 | hypothetical prote |
| 18 | 76 | 7.9 | 744 | 2 A43353 | ascites sialoglyco |
| 19 | 76 | 7.9 | 748 | 2 T47250 | complex I intermed |
| 20 | 75.5 | 7.8 | 638 | 2 T41478 | probable transcrip |
| 21 | 75 | 7.8 | 450 | 2 B97297 | hydrogenase chain |
| 22 | 75 | 7.8 | 857 | 1 A41369 | S-receptor kinase |
| 23 | 74.5 | 7.7 | 384 | 2 S45592 | ERD1 protein - yea |
| 24 | 74.5 | 7.7 | 1101 | 2 T16840 | hypothetical prote |
| 25 | 74 | 7.7 | 377 | 2 JC7535 | chitinase (EC 3.2. |
| 26 | 73.5 | 7.6 | 307 | 2 B95059 | membrane protein [|
| 27 | 73.5 | 7.6 | 307 | 2 A97967 | conserved hypothet |
| 28 | 73 | 7.6 | 304 | 2 A89882 | hypothetical prote |
| 29 | 73 | 7.6 | 679 | 2 B96599 | protein F20N2.12 [|

| | | | | | | |
|-----|------|-----|------|---|--------|---------------------|
| 30 | 73 | 7.6 | 733 | 1 | A46373 | probable serine/th |
| 31 | 72.5 | 7.5 | 243 | 2 | T31144 | hypothetical prote |
| 32 | 72.5 | 7.5 | 408 | 2 | B84518 | hypothetical prote |
| 33 | 72 | 7.5 | 416 | 2 | S75097 | hypothetical prote |
| 34 | 72 | 7.5 | 855 | 2 | T10665 | hypothetical prote |
| 35 | 71.5 | 7.4 | 105 | 2 | T10350 | hypothetical prote |
| 36 | 71.5 | 7.4 | 627 | 2 | B71709 | hypothetical prote |
| 37 | 71 | 7.4 | 227 | 2 | F72334 | conserved hypothet |
| 38 | 71 | 7.4 | 414 | 2 | G71331 | probable cell divi |
| 39 | 71 | 7.4 | 473 | 2 | AF1207 | ABC transporters (|
| 40 | 71 | 7.4 | 480 | 2 | G88690 | protein F41H10.1 [|
| 41 | 71 | 7.4 | 500 | 2 | T10543 | hypothetical prote |
| 42 | 71 | 7.4 | 660 | 2 | T02768 | spike glycoprotein |
| 43 | 70.5 | 7.3 | 188 | 2 | H82933 | hypothetical prote |
| 44 | 70.5 | 7.3 | 412 | 2 | T24023 | hypothetical prote |
| 45 | 70.5 | 7.3 | 424 | 2 | T14525 | S-locus-specific g |
| 46 | 70.5 | 7.3 | 490 | 2 | T32003 | hypothetical prote |
| 47 | 70.5 | 7.3 | 839 | 2 | S54174 | DNA topoisomerase |
| 48 | 70.5 | 7.3 | 906 | 2 | T01440 | hypothetical prote |
| 49 | 70.5 | 7.3 | 1171 | 2 | A42916 | metabotropic gluta |
| 50 | 70.5 | 7.3 | 1548 | 2 | S34583 | serine proteinase |
| 51 | 70.5 | 7.3 | 2718 | 2 | A23475 | G surface protein |
| 52 | 70.5 | 7.3 | 2824 | 2 | T22759 | hypothetical prote |
| 53 | 70 | 7.3 | 513 | 2 | A70378 | histidine kinase s |
| 54 | 70 | 7.3 | 726 | 2 | T08769 | hypothetical prote |
| 55 | 70 | 7.3 | 1072 | 2 | T13156 | KIAA0747 protein - |
| 56 | 69.5 | 7.2 | 315 | 1 | B69812 | ferriochrome ABC tr |
| 57 | 69.5 | 7.2 | 350 | 2 | T39795 | probable ubiquitin |
| 58 | 69.5 | 7.2 | 441 | 2 | C84667 | probable protein k |
| 59 | 69.5 | 7.2 | 573 | 2 | T14096 | methylation enzyme |
| 60 | 69.5 | 7.2 | 574 | 2 | T51799 | CUA1-like protein |
| 61 | 69.5 | 7.2 | 576 | 2 | S26583 | chaperonin hsp60 - |
| 62 | 69.5 | 7.2 | 614 | 2 | H83978 | GTP-binding protei |
| 63 | 69.5 | 7.2 | 768 | 2 | S52684 | probable membrane |
| 64 | 69.5 | 7.2 | 854 | 2 | T14377 | S-receptor kinase |
| 65 | 69.5 | 7.2 | 1180 | 2 | JC2132 | metabotropic gluta |
| 66 | 69.5 | 7.2 | 1212 | 2 | JC2131 | metabotropic gluta |
| 67 | 69.5 | 7.2 | 1706 | 2 | I84499 | zinc finger protei |
| 68 | 69.5 | 7.2 | 2958 | 2 | S64921 | probable membrane |
| 69 | 69.5 | 7.2 | 5376 | 2 | T42215 | zonadhesin - mouse |
| 70 | 69 | 7.2 | 324 | 1 | G1MS | Ig gamma-1 chain C |
| 71 | 69 | 7.2 | 379 | 2 | S46711 | hypothetical prote |
| 72 | 69 | 7.2 | 333 | 1 | G1MSM | Ig gamma-1 chain C |
| 73 | 69 | 7.2 | 444 | 2 | PC4436 | monoclonal antibod |
| 74 | 69 | 7.2 | 446 | 2 | F86107 | anaerobic dicarbox |
| 75 | 69 | 7.2 | 459 | 2 | T27657 | hypothetical prote |
| 76 | 69 | 7.2 | 502 | 2 | T20130 | hypothetical prote |
| 77 | 69 | 7.2 | 694 | 2 | T10565 | hypothetical prote |
| 78 | 69 | 7.2 | 704 | 2 | T50303 | hypothetical prote |
| 79 | 69 | 7.2 | 838 | 2 | T20125 | hypothetical prote |
| 80 | 69 | 7.2 | 2322 | 2 | T10542 | hypothetical prote |
| 81 | 68.5 | 7.1 | 328 | 2 | C81677 | carbohydrate isome |
| 82 | 68.5 | 7.1 | 402 | 2 | T06629 | hypothetical prote |
| 83 | 68.5 | 7.1 | 409 | 2 | S44346 | RAD23 protein homo |
| 84 | 68.5 | 7.1 | 575 | 2 | S29316 | chaperonin 60 - cu |
| 85 | 68.5 | 7.1 | 575 | 2 | S26582 | chaperonin hsp60 - |
| 86 | 68.5 | 7.1 | 653 | 2 | G96675 | hypothetical prote |
| 87 | 68 | 7.1 | 198 | 2 | B89008 | protein W08A12.3 [|
| 88 | 68 | 7.1 | 590 | 2 | S17920 | finger protein zfp |
| 89 | 68 | 7.1 | 794 | 2 | D84765 | similar to mammali |
| 90 | 68 | 7.1 | 810 | 2 | C72785 | probable aldehyde |
| 91 | 68 | 7.1 | 1140 | 2 | T41457 | dna repair protein |
| 92 | 68 | 7.1 | 1203 | 2 | B55094 | chromosomal protei |
| 93 | 68 | 7.1 | 3386 | 1 | GNWVDF | genome polyprotein |
| 94 | 67.5 | 7.0 | 178 | 1 | LGBO | beta-lactoglobulin |
| 95 | 67.5 | 7.0 | 241 | 1 | H81327 | hypothetical prote |
| 96 | 67.5 | 7.0 | 245 | 2 | H69471 | conserved hypothet |
| 97 | 67.5 | 7.0 | 268 | 2 | A71966 | hypothetical prote |
| 98 | 67.5 | 7.0 | 283 | 2 | T24998 | hypothetical prote |
| 99 | 67.5 | 7.0 | 336 | 2 | H72618 | hypothetical prote |
| 100 | 67.5 | 7.0 | 383 | 2 | P96582 | hypothetical prote |

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-539 <ARN>
A;Cross-references: UNIPROT:Q9XON0; GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD3622
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein

Query Match 8.0%; Score 77; DB 2; Length 539;
Best Local Similarity 32.0%; Pred. No. 28;
Matches 24; Conservative 19; Mismatches 20; Indels 12; Gaps 5;

Qy 42 NASVTNSVKGTNAIITWCLGSLIISLAVFVLMFLRKISSEPLKD---EFKNTGSGLLG 98
Db 150 NVSMTKNIK-RNIITFF---LVVCAAAMFTAITETRLTT-PLKLAIVLVENLSHGLV- 202

Qy 99 MANIDLEKSRGDEI 113
Db 203 --NVEIEKIRSKDEI 215

RESULT 16
T21152
hypothetical protein F20E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21152
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19393
A;Accession: T21152
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-357 <WIL>
A;Cross-references: UNIPROT:Q9XV87; EMBL:Z81508; PIDN:CAB04138.1; GSPDB:GNO0023; CESP:F20E11
A;Experimental source: clone F20E11
C;Genetics:
A;Gene: CESP:F20E11.7
A;Map position: 5
A;Introns: 52/3; 88/2; 103/3; 154/3; 190/2; 205/3; 241/2; 270/3; 321/3

Query Match 7.9%; Score 76.5; DB 2; Length 357;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 45; Conservative 33; Mismatches 66; Indels 63; Gaps 10;

Qy 20 ACIPQLRCSNTPPLTCQRYCNAS-----VTNSVKGTNATLWTCGLSLIISLAVF 71
Db 102 SCLPCQ-TCAPPTDPMSEKATCTATPGTDCATLAVKCNINAGFDCNDVALLIQTGG 160

Qy 72 VLMP-----LURKISSEPLKD-----EFKNTGSGLL 96
Db 161 ALPTGTGPGQIAETSVTCGDKIQDPNGIRGNTLIASIASETCLEMTGGLFTSGTGP 220

Qy 97 LGMANIDLEKSR--GDIIL--PRG-----LEYVSECTCEDCIKS-----KPKVDSHCH 143
Db 221 GP1A-----ETSVTCGDDVILQDPNGTRGNTLIASITATQCVSCMQTWRLKRLGRLPQCQC 276

Qy 144 --FPLPAMEGATILVTTKTNDYCKSL 168
Db 277 TAFMDPWPVPEATCTVTGWTSGACATL 303

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-539 <ARN>
A;Cross-references: UNIPROT:Q9XON0; GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD3622
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein

Query Match 8.0%; Score 77; DB 2; Length 539;
Best Local Similarity 32.0%; Pred. No. 28;
Matches 24; Conservative 19; Mismatches 20; Indels 12; Gaps 5;

Qy 42 NASVTNSVKGTNAIITWCLGSLIISLAVFVLMFLRKISSEPLKD---EFKNTGSGLLG 98
Db 150 NVSMTKNIK-RNIITFF---LVVCAAAMFTAITETRLTT-PLKLAIVLVENLSHGLV- 202

Qy 99 MANIDLEKSRGDEI 113
Db 203 --NVEIEKIRSKDEI 215

RESULT 16
T21152
hypothetical protein F20E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21152
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19393
A;Accession: T21152
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-357 <WIL>
A;Cross-references: UNIPROT:Q9XV87; EMBL:Z81508; PIDN:CAB04138.1; GSPDB:GNO0023; CESP:F20E11
A;Experimental source: clone F20E11
C;Genetics:
A;Gene: CESP:F20E11.7
A;Map position: 5
A;Introns: 52/3; 88/2; 103/3; 154/3; 190/2; 205/3; 241/2; 270/3; 321/3

Query Match 7.9%; Score 76.5; DB 2; Length 357;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 45; Conservative 33; Mismatches 66; Indels 63; Gaps 10;

Qy 20 ACIPQLRCSNTPPLTCQRYCNAS-----VTNSVKGTNATLWTCGLSLIISLAVF 71
Db 102 SCLPCQ-TCAPPTDPMSEKATCTATPGTDCATLAVKCNINAGFDCNDVALLIQTGG 160

Qy 72 VLMP-----LURKISSEPLKD-----EFKNTGSGLL 96
Db 161 ALPTGTGPGQIAETSVTCGDKIQDPNGIRGNTLIASIASETCLEMTGGLFTSGTGP 220

Qy 97 LGMANIDLEKSR--GDIIL--PRG-----LEYVSECTCEDCIKS-----KPKVDSHCH 143
Db 221 GP1A-----ETSVTCGDDVILQDPNGTRGNTLIASITATQCVSCMQTWRLKRLGRLPQCQC 276

Qy 144 --FPLPAMEGATILVTTKTNDYCKSL 168
Db 277 TAFMDPWPVPEATCTVTGWTSGACATL 303

RESULT 17
T19277
hypothetical protein C14B4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19277; T19909
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19100
A;Accession: T19277
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1404 <WIL>
A;Cross-references: UNIPROT:O45251; EMBL:Z81471; PIDN:CAB03966.1; GSPDB:GNO0023; CESP:C14B4.2
A;Experimental source: clone C14B4
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19194
A;Accession: T19909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1404 <WIL>
A;Cross-references: EMBL:Z81483; PIDN:CAB03966.1; GSPDB:GNO0023; CESP:C14B4.2
A;Experimental source: clone C43D7
C;Genetics:
A;Gene: CESP:C14B4.2
A;Map position: 5
A;Introns: 175/1; 209/3; 304/2; 482/3; 611/3; 680/1; 787/1; 1048/3; 1112/2; 1197/2; 1237/2; 1237/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C14B4.2

Query Match 7.9%; Score 76.5; DB 2; Length 1404;
Best Local Similarity 24.8%; Pred. No. 81;
Matches 35; Conservative 21; Mismatches 56; Indels 29; Gaps 6;

Qy 2 LQWAGCCSQNEYFDSLH--ACIPQLRCSNTPPLTCQRYC-----NASVTN-SVKGTNA 54
Db 77 LLESGFCHVTEQFDLVLQDSAHFFGNSRTEAHVRLTCKGYCTVGSGMTVTDLSIYYRNE 136

Qy 55 ILWTCGLSLIISLAVFVLMFLRKISSRPLKDEFKNTG-----SGLIGMANIDLEKSRGT 110
Db 137 LIITCTGKVLVIG-----DSDVITCFRNDALWQVEKLNKMTGTSIEQSEDG 183

Qy 111 DEILPRGLEVTVECTCEDC 131
Db 184 TIFV-----KYSMNIVLHEDC 199

RESULT 18
A43353
ascites sialoglycoprotein-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43353
R;Sheng, Z.; Wu, K.; Carraway, K.L.; Fregien, N.
J. Biol. Chem. 267, 16341-16346, 1992
A;Title: Molecular cloning of the transmembrane component of the 13762 mammary adenocarcinoma
A;Reference number: A43353; MUID:92355597; PMID:1379596
A;Accession: A43353
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-744 <SHE>
A;Cross-references: UNIPROT:Q63661
A;Experimental source: mammary adenocarcinoma
A;Note: sequence extracted from NCBI backbone (NCBI:110690, NCBI:110691)
C;Keywords: glycoprotein
F;655-694/Domain: EGF homology <EGF>

Query Match 7.9%; Score 76; DB 2; Length 744;
Best Local Similarity 22.1%; Pred. No. 47;
Matches 34; Conservative 29; Mismatches 57; Indels 34; Gaps 6;

Qy 4 MAGCCSQNEYFDSLHACIPQLRCSNTPPLTCQRYC-----NASVTNSVKGT 52

Db 49 LGRTRAGTDSANATNFIAFAAQYNTSSLSKSPITVQMFLEPNDIRVVHNNQTVAFNTSDT 108
QY 53 NAI-LWTCGLSLI-----ISLAVFLMFLFKISSEPLKDFKNTGSGLLG 98
Db 109 EDLPVFNATGVLLIQSGVSQVAFDGTVTISVIALSNILHASSS--LSEBYRNHTKGLLG 166
QY 99 MANIDLEKSTGTDEIILPRGLETVTVECTEDCI 132
Db 167 VWNDNPE-----DQFRMPNG--STIPSTNTSEETL 193
RESULT 19
T47250
complex I intermediate-associated protein CIA84 precursor, mitochondrial [imported] - Ne
C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47250
R;Kuffner, R.; Rohr, A.; Schmiede, A.; Krull, C.; Schulte, U.
J. Mol. Biol. 283, 409-17, 1998
A;Title: Involvement of two novel chaperones in the assembly of mitochondrial NADH:Ubiqu
A;Reference number: 222191; MUID:9769214; PMID:9769214
A;Accession: T47250
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-748 <KOE>
A;Cross-references: UNIPROT:O42637; EMBL:AJ001712; PIDN:CAA04945.1
C;Genetics:
A;Gene: cia84
A;Genome: nuclear
A;Introns: 693/2
C;Function:
A;Description: required for complex I membrane arm assembly
C;Superfamily: Neurospora crassa complex I intermediate-associated protein CIA84
C;Keywords: mitochondrion
F;1-20/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;1-748/Product: complex I intermediate associated protein CIA84 #status predicted <MA
Query Match 7.9%; Score 76; DB 2; Length 748;
Best Local Similarity 25.5%; Pred. No. 47;
Matches 27; Conservative 20; Mismatches 49; Indels 10; Gaps 2;
QY 82 SEPLKDFKNTGSGLLGMANIDLEKSTGTDEIILPRGLETVTVECTEDCIKPKVDSD 141
Db 266 SKPIHGSPGTGLLELVRSRRSRQKNWLLP-----VFEVQVQDFAKKGLDAF 319
QY 142 HCPPLPAMEG---ATILVTNTDCKSLPAALGATEIEKISA 183
Db 320 LQSVLADKGPQGIKTYLQTMASGDFYQSHSVKVDATTINRLMQA 365
RESULT 20
T41478
probable transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41478
R;Bothe, G.; Pohl, T.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A;Reference number: 221997
A;Accession: T41478
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-638 <BOT>
A;Cross-references: UNIPROT:O74910; EMBL:AL031644; PIDN:CAA21064.1; GSPDB:GN00068; SPDB:
C;Genetics:
A;Experimental source: strain 972h-; cosmid c613
A;Gene: SPDB:SPCC613.12c
A;Map position: 3
C;Superfamily: Schizosaccharomyces pombe probable transcription regulator SPCC613.12c
Query Match 7.8%; Score 75.5; DB 2; Length 638;
Best Local Similarity 22.74%; Pred. No. 45;
Matches 44; Conservative 20; Mismatches 61; Indels 69; Gaps 7;

QY 12 EYDSSLHACIPQQLRCSSNTPLTCORYCNASVTNSVKGNTNAILWTCLGLSLIISLAVF 71
Db 42 EYDYPYRAELPCP-----KPSLSISKHSIAKVPNSVNRK-----LEQLLLTSQTF 88
QY 72 VLMFLARKISSEPLKDFKNTGSGLLGMANIDLEKSTGTDEIILPRGLETVTVEEC----- 126
Db 89 L-----PNSRPYLSEVRVKHTL-----LSNSITGDKPSLIHVDTPBECFLQE 134
QY 127 -----TCEDCIKSPKVDSDHCFPLPAMEGATILVT 158
Db 135 AKLFGPVNSQFNDAVSTHISPLPRAVEDC-----QKFEIDNPSLSPVDKHGAIIIRT 190
QY 159 TKTN-----DYCKS 167
Db 191 YKKNKLLPDYLS 204
RESULT 21
B97297
hydrogenase chain (ferredoxin) [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97297
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <KUR>
A;Cross-references: UNIPROT:Q97B85; GB:AE001437; PIDN:AAK81165.1; PID:gl5026303; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3230
Query Match 7.8%; Score 75; DB 2; Length 450;
Best Local Similarity 20.5%; Pred. No. 35;
Matches 42; Conservative 23; Mismatches 72; Indels 68; Gaps 9;
QY 15 DSSLHACIPQQLRCSSNTPLTCORYC--NASVTNSVKGNTNAIL-----LWTCGLG 61
Db 74 DNIVEKIKEDSSCHSNEGETPCQKSCPFDAIILVDKNTKTSIQDLCTDCGNCITSCPS 133
QY 62 LSLIISLAVFLMFLARKISSEPLKDFKNTGSGLLGMA-----NIDLEKSR----- 109
Db 134 GS-----ILDKIEFMEPLNFKNNETVIAAVAPAIAGQFGENVSLMLRTAFK 181
QY 110 -----GDEIILPRGLETV-----VEECTCEDCIKSPKVDSD---HC 143
Db 182 KVGFDADVEVAFPADMLTIKEAFEPNELVNSKDDLMITSCCPMWVSMIRKIYKDLARHV 241
QY 144 FP--LPAMEGATILVTNTDYCK 166
Db 242 SPVSVPMIASGRVI---KKLNPCK 263
RESULT 22
A41369
S-receptor kinase (EC 2.7.1.-) 6 precursor - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 11-Jun-1999
C;Accession: A41369
R;Stein, J.C.; Howlett, B.; Boyes, D.C.; Nasrallah, M.E.; Nasrallah, J.B.
Proc. Natl. Acad. Sci. U.S.A. 88, 8816-8820, 1991
A;Title: Molecular cloning of a putative receptor protein kinase gene encoded at the self
A;Reference number: A41369; MUID:92020942; PMID:1681543
A;Accession: A41369
A;Molecule type: DNA
A;Residues: 1-857 <STE>
A;Cross-references: GB:M76647; NID:gl67166; PIDN:AAA33000.1; PID:gl67167.

A;Experimental source: S6S6 homozygote kale

C;Genetics:

A;Gene: SRK

A;Note: locus is highly polymorphic

C;Function:

A;Description: involved in preventing fertilization between plants having the same S-locus
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein
C;Keywords: ATP; glycoprotein; magnesium; phosphotransferase; receptor; serine/threonine
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-857/Product: S-receptor kinase #status predicted <MA>
F;41-436/Domain: S-locus-specific glycoprotein homology <SSG>
F;447-466/Domain: transmembrane #status predicted <TM>
F;526-813/Domain: protein kinase homology <KIN>
F;534-542/Region: protein kinase ATP-binding motif

F;47,120,196,260,314,389,442/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;556,572,653,655/Active site: Lys, Glu, Asp, Lys #status predicted
F;659,662/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 7.8%; Score 75; DB 1; Length 857;

Best Local Similarity 17.6%; Pred. No. 67;

Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

Qy 24 COLRCSSNPPLTCQRYCNASVTNSVKGTHAILWT----- 58

Db 380 CKKRCISD---CNCATFANADIRNG--GSGCVIWERLEDIRNVATDAIDGQDIYVRLAA 434

Qy 59 -----CLGLSLIIISLAVFLVLMFLIRKISSEPLKDEPKNTGSGLLGMANIDLEK 106

Db 435 ADIAKRNASGKIISLTGVSVLLIMFCL-----WKKKQKRAKASALSIAINTQNRQ 487

Qy 107 SRTGDEIILPGLRYTVEECTCECIKSPKVDSDHCP-----PLPAMEGATILVTYTKT 161

Db 488 NLPNEMVL-----SSKREFSGEYKFEELPLIEME---TVVKATEN 527

Qy 162 NDYCKSL 168

Db 528 FSSCNKL 534

RESULT 23

S45592

ERD1 protein - yeast (Kluyveromyces marxianus var. lactis)

C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica

C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S45592

R;Dean, N.

Yeast 10, 1117-1124, 1994

A;Title: Cloning and DNA sequence of a Kluyveromyces lactis ERD1 homologue.

A;Reference number: S45592; MUID:95084639; PMID:7992512

A;Accession: S45592

A;Molecule type: DNA

A;Residues: 1-384 <DEA>

A;Cross-references: UNIPROT:P41771; EMBL:U04714; NID:9436876; PIDN:AAA21530.1; PID:94368

A;Note: the source is designated as Kluyveromyces lactis

C;Genetics:

A;Gene: ERD1

Query Match 7.7%; Score 74.5; DB 2; Length 384;

Best Local Similarity 27.2%; Pred. No. 33;

Matches 43; Conservative 21; Mismatches 55; Indels 39; Gaps 8;

Qy 9 SONEFYFSLHACIPCOLRCSSNPPLTCQRYCNASVTNSVKGTHAILWTCLGLSLIISL 68

Db 67 SSLKLFKISRVIIIPWQLVC-----IILFYQY---SPTNNV---SNKLLWFFLNVSPLEL 115

Qy 69 AVFVLMFLRKISSEPLKDEPKNTGSGLLGMANIDLEKSGTGEIILPGLRYTVEECTC 128

Db 116 -FYFAMILR--SSAMVARCFKR-----ILWVADIEPKPYRNYYIISDTLTSY----- 161

Qy 129 EDCKSKPKVDSDHCFPLPAMEGATILVTYTKNDYCK 166

Db 162 -----SKFLVD-----LAIYATFLFHDPTNVKQ 185

RESULT 24

T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T16840

R;Geisel, C.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid T10E10.

A;Reference number: Z18588

A;Accession: T16840

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1101 <GEI>

A;Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:g1049343; PIDN:AAA803

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T10E10.4

A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 76/3;

Query Match 7.7%; Score 74.5; DB 2; Length 1101;

Best Local Similarity 36.7%; Pred. No. 96;

Matches 18; Conservative 11; Mismatches 15; Indels 5; Gaps 3;

Qy 7 QCSQNEYFDSLLHACIPCOLR--CSSNTPLTCQRYCNASVTNSVKGTH 53

Db 350 QCSQSTVFNSDLNVCVPLAIQNSDSSTQPPVCS--C-SQVSSSCPCTS 395

RESULT 25

JC7535

chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus

C;Species: Streptomyces thermoviolaceus

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C;Accession: JC7535

R;Tsujibo, H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.; Inanomi

Biosci. Biotechnol. Biochem. 64, 2445-2453, 2000

A;Title: Family 19 chitinases from Streptomyces thermoviolaceus OPC-520: Molecular cloning

A;Reference number: JC7535; MUID:21036907; PMID:11193414

A;Accession: JC7535

A;Molecule type: DNA

A;Residues: 1-377 <TSU>

A;Cross-references: UNIPROT:Q9RHU5; DBJ:AB016842

A;Experimental source: strain OPC-520

C;Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation

lysaccharide-binding domain that is important in the efficient hydrolysis of insoluble chitin

C;Genetics:

A;Gene: chi35

C;Keywords: glycosidase; hydrolase

Query Match 7.7%; Score 74; DB 2; Length 377;

Best Local Similarity 27.0%; Pred. No. 36;

Matches 31; Conservative 11; Mismatches 23; Indels 50; Gaps 6;

Qy 47 NSVKGTHAILWTCLGLS-----LIISLAVFLVLMF-----L 76

Db 138 NSANGTRVQIWTCTGGSNQKNAPATGGSTPAPSGFVVSEAQFNQMFNRPFTYVQGL 197

Qy 77 LRKISSEPLKDEPKNTG-----SGLGMANIDLEKSGTGEIILPGLRYTVE 124

Db 198 VQALSAPP---GPANTGDDTTKKQEAFLANVNH---TG-----GLQYVVE 239

RESULT 26

B95099

membrane protein [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: B95099

R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Mayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <KUR>
A;Cross-references: UNIPROT:Q97RG2; UNIPROT:Q8DQB0; GB:AE005672; PIDN:AAK74987.1; PID:gl
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0859

Query Match 7.6%; Score 73.5; DB 2; Length 307;
Best Local Similarity 26.2%; Pred. No. 33;
Matches 48; Conservative 26; Mismatches 60; Indels 49; Gaps 12;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCN-ASVTNSVK-GTNAILWT 58
Db 1 MTELAKQLLE-----LTYIVIGCQFLHTA-----YCSYKDKTNPVRIGTSA-FWT 44
QY 59 CIGLSLI-----ISLAVFLMFLRL-----KISSEPLKDFKNTGSGLLGMANIDLE 105
Db 45 LLSITFIGGSMYMNMSIGIIVILLSLTLFKQVRIGTLPISLDEWK-----ANI--E 93

QY 106 KSRGTGDEIILPRGLEIYVTEBCTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYC 165
Db 94 SNRLKNKIFIPVML-MAILALVLAQMPIEFSKIS----ISLAL--PATISVLVITNSHP 146

QY 166 KSL 168
Db 147 KSL 149

RESULT 27
A97967
conserved hypothetical protein spr0761 [imported] - *Streptococcus pneumoniae* (strain R6)
C;Species: *Streptococcus pneumoniae*
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
A;Accession: A97967
R;Authors: J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A97967
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <KUR>
A;Cross-references: UNIPROT:Q97RG2; UNIPROT:Q8DQB0; GB:AE007317; PIDN:AAK99565.1; PID:gl
C;Genetics:
A;Gene: spr0761

Query Match 7.6%; Score 73.5; DB 2; Length 307;
Best Local Similarity 26.2%; Pred. No. 33;
Matches 48; Conservative 26; Mismatches 60; Indels 49; Gaps 12;

QY 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCN-ASVTNSVK-GTNAILWT 58
Db 1 MTELAKQLLE-----LTYIVIGCQFLHTA-----YCSYKDKTNPVRIGTSA-FWT 44
QY 59 CIGLSLI-----ISLAVFLMFLRL-----KISSEPLKDFKNTGSGLLGMANIDLE 105
Db 45 LLSITFIGGSMYMNMSIGIIVILLSLTLFKQVRIGTLPISLDEWK-----ANI--E 93

QY 106 KSRGTGDEIILPRGLEIYVTEBCTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKNDYC 165
Db 94 SNRLKNKIFIPVML-MAILALVLAQMPIEFSKIS----ISLAL--PATISVLVITNSHP 146

QY 166 KSL 168
Db 147 KSL 149

Db 147 KSL 149

RESULT 28
A89882
hypothetical protein ctab [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A;Accession: A89882
R;Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89882
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <KUR>
A;Cross-references: UNIPROT:Q99UV7; GB:BA000018; PID:gl3700917; PIDN:BA842213.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: ctab
C;Superfamily: heme O synthase

Query Match 7.6%; Score 73; DB 2; Length 304;
Best Local Similarity 23.8%; Pred. No. 36;
Matches 24; Conservative 16; Mismatches 29; Indels 32; Gaps 4;

QY 2 LQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKGTNAILWTCLG 61
Db 67 LINGGACALNNYYDDIDRIMPSK---QNRP-----TVNNRITDQNLILLUS-FG 111
QY 62 LSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANI 102
Db 112 MMLVGSICIFLL-----NIPSGVIGLMCI 135

RESULT 29
B96599
protein P20N2.12 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A;Accession: B96599
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.E.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-679 <STO>
A;Cross-references: UNIPROT:Q9ZWD7; GB:AE005173; MID:g8778489; PIDN:AAF79497.1; GSPDB:G
C;Genetics:
A;Gene: F20N2.12
A;Map position: 1

Query Match 7.6%; Score 73; DB 2; Length 679;
Best Local Similarity 22.2%; Pred. No. 81;
Matches 35; Conservative 21; Mismatches 58; Indels 44; Gaps 8;

QY 7 QCSQNEYFDSLHACIPQ----LRCSNTP-----PLTCQRYC 41
Db 199 KCQTNLQEVYVH-CSICKENLTCARNPPLSTISHLSKSHHEPLSFPPRIPLPDCA-C 256
QY 42 NASVTNSVKGTNAILWTCLGSLIISLAVFLMFLRL-----KISSEPLKDFKNTGSG 95

A: Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* **g.**

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75097

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-416 <KAN>

A;Cross-references: UNIPROT:P73895; EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA1795

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: Synchocystis hypotheical protein sll0243

Query Match 7.5%; Score 72; DB 2; Length 416;
Best Local Similarity 21.2%; Pred. No. 61;
Matches 48; Conservative 30; Mismatches 60; Indels 88; Gaps 10;

QY 9 SNEYFDSLHACIPQ-----LRCSNTPPLTCQRYC-----NASVT 46

Db 167 SRIQASLILHQPVLPSISIEDLQAYDNVTEYDQRYLFSIHFLPQSLQIDOSTFL 226

QY 47 NSVK-----GTNAILWTCLGSLIIS-----LAVFLMF-----LLR 78

Db 227 NTKRLTORLIESDGDKIATWSGLFLSLHRRCLILAILGYNETHLLGRQGALLI 286

QY 79 KISSEPLKDFKNTGSGLLGMANIDLEKS-RTGDEIILPRGLETYTVEECTCEDCIKSKPK 137

Db 287 RAENSLWFFDIDPSNGLVSVSISLDKAYELDELFTFVG-----KPY 330

QY 138 VD-----SDHCFPLPAMEEGATILVTTKNDYCKSLPAAL 172

Db 331 IDSYSQSLGTQTSSSLEPLP---GAS-----TPNYCQACHQSL 366

RESULT 34

T10665

hypotheical protein F6E21.30 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T10665

R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16533

A;Accession: T10665

A;Molecule type: DNA

A;Residues: 1-855 <BEV>

A;Cross-references: UNIPROT:Q9M091; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.30

A;Experimental source: cultivar Columbia; BAC clone F6E21

C;Genetics:

A;Gene: ATSP:F6E21.30

A;Map position: 4

A;Introns: 345/1; 756/2

C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prob

Query Match 7.5%; Score 72; DB 2; Length 855;

Best Local Similarity 21.5%; Pred. No. 1.3e+02;

Matches 37; Conservative 24; Mismatches 73; Indels 38; Gaps 6;

QY 7 QCSNEYFDSLHAC-----IPQLRCSSNTPPLTCQRYCNASVTSVNGTNAIWL 57

Db 282 QTSNRSLDSLALACKDREDYRNTNLERKTCGRITISYANGCTGYGTGNPVLN 341

QY 58 TGLGLSLIISLAVFV-----LMLLRKISSEPLKDFKNTGSGLLGMANID-----LEK 106

Db 342 GCKGAGTGFGVLVGLWGLWLRKFLKRIITKRRKPKFKRNG-GLLILQLNLNREGVVEK 400

QY 107 SRT-----GDEIILPRGLETYTVEECTCED-----CIKSKPKVDS 141

Db 401 TRVNSRELEKATENFSENRLVHGQGTGYKGLMDGRTVAVKSKVIDED 452

RESULT 35

T10350

hypotheical protein 81 - Orgyia pseudotsugata nuclear polyhedrosis virus

C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 12-Jun-2003

C;Accession: T10350

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

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A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: F72334

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: F72334

hypothetical protein F313.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10543
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17080
A;Accession: T10543
A;Molecule type: DNA
A;Residues: 1-500 <BEV>
A;Cross-references: UNIPROT:Q95V26; EMBL:AL080237; GSPDB:GN00062; ATSP:F313.50
A;Experimental source: cultivar Columbia; BAC clone F313
C;Genetics:
A;Gene: ATSP:F313.50
A;Map position: 4

Query Match 7.4%; Score 71; DB 2; Length 500;
Best Local Similarity 23.6%; Pred. No. 91;
Matches 33; Conservative 17; Mismatches 52; Indels 38; Gaps 7;

Qy 16 SLHA-----CIPQLRCSSNPPLTCQRYCNASVTNS-----VKGTNAILWTCLG 61
Db 142 SLHSGKEVHGFCLRNKLCIDAYVATLDMYKSGDLQSAIBTFWGIKNKSLASWNCML 201

Qy 62 LSLII-----SLAVFVFLRLKISSEPLKDEF-----KNTGSLGLGMANIDLEKSR 108
Db 202 MGYAMFGREGIEAFAFVML---EAGMEPDAITFTSVLSCKNSGLVQEGWKYFDLMRSR 258

Qy 109 TGDIEILPRGLEVTVERCTC 128
Db 259 YG---IIP-----TIEHCSC 270

RESULT 42
T02768
spike glycoprotein G homolog - Adelaide River virus
C;Species: Adelaide River virus
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T02768
R;Wang, Y.; Walker, P.J.
Virology 195, 719-731, 1993
A;Title: Adelaide river rhabdovirus expresses consecutive glycoprotein genes as polycist
A;Reference number: Z14732; MUID:9331730; PMID:8337841
A;Accession: T02768
A;Molecule type: genomic RNA
A;Status: translated from GB/EMBL/DBJ
A;Residues: 1-660 <WAN>
A;Cross-references: UNIPROT:Q89669; EMBL:L09206; NID:g348027; PIDN:AAA02762.1; PID:g3480
A;Experimental source: isolate DPP61
C;Superfamily: rhabdovirus spike glycoprotein G

Query Match 7.4%; Score 71; DB 2; Length 660;
Best Local Similarity 32.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 13; Mismatches 22; Indels 2; Gaps 2;

Qy 57 WTCIGSLIISL-AVFVFLRLKISSEPLKDEFKNT-GSGLGLGMANIDLEKSR 109
Db 558 WTWGVCLFSIFLYKIIMLRKHSNDNVKFEKTAGKVMIGQPIDTKSMRT 612

RESULT 43
H82933
hypothetical protein UUI01 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82933
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: H82933
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-188 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30507.1; GSPDB:GN001:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UUI01
A;Genetic code: SGC3

Query Match 7.3%; Score 70.5; DB 2; Length 188;
Best Local Similarity 25.5%; Pred. No. 37;
Matches 27; Conservative 19; Mismatches 39; Indels 21; Gaps 4;

Qy 51 GTWAILWTCLGLSLIISLAVFV---LWFLRLKISSEPLKDEFKNTGSLGLGMANIDLEKS 107
Db 35-GDEAYKTSGLSGSELYINADFESTNILDUKBELQAKIDAFILISNDITVLDLSEVFLDIH 94

Qy 108 RTGDEIILPRGLEVTVERCTCED-----CIKSPKPKVDSDHC 143
Db 95 FSEDD-----DYE-EDCCDECCDENEACCNSEKVEECC 132

RESULT 44
T24023
hypothetical protein R07B7.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T24023
R;Harris, B.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19830
A;Accession: T24023
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-412 <WIL>
A;Cross-references: UNIPROT:Q21806; EMBL:Z75955; PIDN:CAB00125.1; GSPDB:GN00023; CESP:RO
A;Experimental source: clone R07B7
C;Genetics:
A;Gene: CESP:R07B7.16
A;Map position: 5
A;Introns: 26/3; 53/3; 89/1; 139/3; 203/2; 325/1
C;Superfamily: erba transforming protein homology

Query Match 7.3%; Score 70.5; DB 2; Length 412;
Best Local Similarity 19.6%; Pred. No. 83;
Matches 36; Conservative 32; Mismatches 69; Indels 47; Gaps 9;

Qy 11 NEYFDSLHLHACIPQLRCSSNPPLTCQRYCNASVTNSVKGTVNAILWTCLGLSLIISLAV 70
Db 186 NPVFDs---SRIPNLTPVSNKAPKLCIMTYMHSALLAAVEASKT-----PEFFSKISH 235

Qy 71 FVLMFLRLKISSEPLKDEFKNTGSGLLGMANIDLEKSRRTGDEIILPRGLEY-TVEECTCE 129
Db 236 EARMILIRHVS�-----IGSNMMS-ASPSMH-HRKSDELLPDGTVFGSIGGLAS 284

Qy 130 DC---IKSPKVDSD-HCF-----PLPAMEGATILVTTKNDY 164
Db 285 EVLGEIKYKNQLOOILHAFILRNVDREYVMILKAILMRNPSVPLGLTDOLIENERNQY 344

Qy 165 CKSL 168
Db 345 AKAL 348

RESULT 45
T14525
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14525
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class
mechanism.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:44:33 ; Search time 214.385 Seconds
(without alignments)
493.825 Million cell updates/sec

Title: US-10-077-137-1
Perfect score: 964
Sequence: 1 MLOMACQCSQNEFYDSLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1 | 964 | 100.0 | 184 | 1 | TR17 HUMAN |
| 2 | 960 | 99.6 | 184 | 2 | Q6P546 |
| 3 | 960 | 99.6 | 184 | 2 | AAHS8291 |
| 4 | 572 | 59.3 | 185 | 1 | TR17 MOUSE |
| 5 | 116.5 | 12.1 | 175 | 1 | T13C MOUSE |
| 6 | 116.5 | 12.1 | 175 | 2 | Q8R4W8 |
| 7 | 94 | 9.8 | 323 | 1 | TNR6 BOVIN |
| 8 | 93 | 9.6 | 184 | 1 | T13C HUMAN |
| 9 | 92.5 | 9.6 | 334 | 2 | Q6VT98 |
| 10 | 92.5 | 9.6 | 334 | 2 | AA547559 |
| 11 | 89 | 9.2 | 3005 | 2 | Q6BFG4 |
| 12 | 88.5 | 9.2 | 217 | 2 | Q97D61 |
| 13 | 86.5 | 9.0 | 804 | 2 | Q80XB3 |
| 14 | 86.5 | 9.0 | 809 | 2 | Q80XB2 |
| 15 | 86.5 | 9.0 | 823 | 2 | Q80XB6 |
| 16 | 86.5 | 9.0 | 827 | 2 | Q8CDK8 |
| 17 | 86.5 | 9.0 | 834 | 2 | Q8BH12 |
| 18 | 86.5 | 9.0 | 842 | 2 | Q8R056 |
| 19 | 86.5 | 9.0 | 867 | 1 | PML1 MOUSE |
| 20 | 86 | 8.9 | 1309 | 2 | Q6CCL1 |
| 21 | 85.5 | 8.9 | 1193 | 2 | Q9YLX8 |
| 22 | 83.5 | 8.7 | 938 | 2 | Q8RWV7 |
| 23 | 83.5 | 8.7 | 1998 | 2 | Q9STR8 |
| 24 | 83 | 8.6 | 449 | 2 | Q8C8R5 |
| 25 | 83 | 8.6 | 474 | 2 | Q8C9L4 |
| 26 | 82.5 | 8.6 | 164 | 2 | Q7RAA5 |
| 27 | 82.5 | 8.6 | 1142 | 2 | Q6CCL7 |
| 28 | 82 | 8.5 | 327 | 2 | Q97491 |
| 29 | 82 | 8.5 | 967 | 2 | Q8C2G0 |
| 30 | 82 | 8.5 | 1009 | 1 | FAK2 MOUSE |
| 31 | 82 | 8.5 | 1009 | 1 | FAK2 RAT |

ALIGNMENTS

| | | | | | |
|-----|------|-----|------|---|------------|
| 32 | 81.5 | 8.5 | 314 | 2 | Q8VEV6 |
| 33 | 81.5 | 8.5 | 2233 | 2 | Q94711 |
| 34 | 81 | 8.4 | 595 | 2 | Q39191 |
| 35 | 81 | 8.4 | 773 | 2 | O01892 |
| 36 | 80.5 | 8.4 | 314 | 2 | Q7TQO9 |
| 37 | 80.5 | 8.4 | 487 | 2 | Q8IN99 |
| 38 | 80 | 8.3 | 735 | 2 | O81820 |
| 39 | 79.5 | 8.2 | 153 | 2 | Q8KLY1 |
| 40 | 79.5 | 8.2 | 1009 | 1 | FAK2 HUMAN |
| 41 | 79.5 | 8.2 | 1009 | 2 | Q6PID4 |
| 42 | 79.5 | 8.2 | 1009 | 2 | AAH36651 |
| 43 | 79.5 | 8.2 | 1299 | 2 | Q26489 |
| 44 | 79 | 8.2 | 333 | 2 | Q7R6V0 |
| 45 | 79 | 8.2 | 1200 | 2 | Q802S1 |
| 46 | 78.5 | 8.1 | 293 | 1 | T13X HUMAN |
| 47 | 78.5 | 8.1 | 314 | 2 | Q8VFW0 |
| 48 | 78.5 | 8.1 | 343 | 1 | MJK2 METJA |
| 49 | 78.5 | 8.1 | 485 | 2 | Q9HG77 |
| 50 | 78.5 | 8.1 | 522 | 2 | Q8NGT0 |
| 51 | 78.5 | 8.1 | 789 | 2 | O8LQ43 |
| 52 | 78 | 8.1 | 841 | 2 | O8R221 |
| 53 | 77.5 | 8.0 | 738 | 2 | O81819 |
| 54 | 77.5 | 8.0 | 738 | 2 | Q9LWN6 |
| 55 | 77.5 | 8.0 | 853 | 2 | Q9YKU7 |
| 56 | 77.5 | 8.0 | 968 | 2 | O04623 |
| 57 | 77 | 8.0 | 249 | 1 | T13X MOUSE |
| 58 | 77 | 8.0 | 399 | 2 | Q6BU93 |
| 59 | 77 | 8.0 | 522 | 2 | Q9M3B3 |
| 60 | 77 | 8.0 | 539 | 2 | Q9XON0 |
| 61 | 77 | 8.0 | 2149 | 2 | Q6CSU4 |
| 62 | 76.5 | 7.9 | 357 | 2 | Q9XV87 |
| 63 | 76.5 | 7.9 | 656 | 2 | Q9FJ83 |
| 64 | 76.5 | 7.9 | 1404 | 2 | O45251 |
| 65 | 76 | 7.9 | 465 | 2 | O6LHF6 |
| 66 | 76 | 7.9 | 465 | 2 | CAG23274 |
| 67 | 76 | 7.9 | 566 | 2 | Q7NBH6 |
| 68 | 76 | 7.9 | 748 | 1 | C184_NEUCR |
| 69 | 76 | 7.9 | 759 | 2 | Q7S820 |
| 70 | 76 | 7.9 | 797 | 2 | Q872A6 |
| 71 | 76 | 7.9 | 1255 | 2 | Q7RM66 |
| 72 | 76 | 7.9 | 1805 | 2 | Q63661 |
| 73 | 75.5 | 7.8 | 191 | 2 | Q7QOR6 |
| 74 | 75.5 | 7.8 | 202 | 2 | Q8D6L4 |
| 75 | 75.5 | 7.8 | 454 | 2 | Q76NX0 |
| 76 | 75.5 | 7.8 | 454 | 2 | AAO93326 |
| 77 | 75.5 | 7.8 | 476 | 2 | Q6FQJ9 |
| 78 | 75.5 | 7.8 | 567 | 2 | O8JKV7 |
| 79 | 75.5 | 7.8 | 638 | 1 | YCSB_SCHPO |
| 80 | 75 | 7.8 | 450 | 2 | Q97EB5 |
| 81 | 75 | 7.8 | 706 | 2 | Q8GH21 |
| 82 | 75 | 7.8 | 718 | 2 | Q9BI07 |
| 83 | 75 | 7.8 | 849 | 1 | SRK6 BRAOL |
| 84 | 75 | 7.8 | 920 | 2 | Q6FK14 |
| 85 | 75 | 7.8 | 985 | 2 | Q7Z5T8 |
| 86 | 75 | 7.8 | 985 | 2 | Q8IZ06 |
| 87 | 75 | 7.8 | 1193 | 2 | Q6FKT2 |
| 88 | 75 | 7.8 | 1569 | 2 | Q6W4X9 |
| 89 | 75 | 7.8 | 1569 | 2 | AAQ82434 |
| 90 | 74.5 | 7.7 | 263 | 2 | Q8C3K1 |
| 91 | 74.5 | 7.7 | 384 | 1 | ERD1_KULJA |
| 92 | 74.5 | 7.7 | 521 | 2 | Q7ZTM1 |
| 93 | 74.5 | 7.7 | 660 | 2 | Q7QV47 |
| 94 | 74.5 | 7.7 | 853 | 2 | Q9YKV7 |
| 95 | 74.5 | 7.7 | 966 | 2 | Q22378 |
| 96 | 74.5 | 7.7 | 2199 | 2 | Q7QTX2 |
| 97 | 74 | 7.7 | 353 | 2 | Q8KMK7 |
| 98 | 74 | 7.7 | 377 | 2 | Q9RHU5 |
| 99 | 74 | 7.7 | 789 | 2 | Q91000 |
| 100 | 74 | 7.7 | 2371 | 2 | Q8NFY8 |

| | |
|-----------|--------------|
| Q8vev6 | mus musculus |
| Q94711 | paramedius |
| Q39191 | arabidopsis |
| O01892 | caenorhabdi |
| Q7tcq9 | mus musculus |
| O8in99 | drosohila |
| O81820 | arabidopsis |
| Q8kly1 | pseudomonas |
| Q14289 | h protein t |
| Q6pid4 | homo sapien |
| Aah36651 | homo sapi |
| Q26489 | spodoptera |
| Q7r6v0 | plasmodium |
| Q802s1 | fugu rubrip |
| O81819 | mus musculus |
| Q8vfw0 | mus musculus |
| O58752 | methanococ |
| Q9hg77 | homo sapien |
| Q8n6t0 | homo sapien |
| Q8lq43 | oryza sativ |
| Q8r221 | mus musculus |
| O81819 | arabidopsis |
| Q9lmw6 | arabidopsis |
| Q9yku7 | human immun |
| O04623 | arabidopsis |
| Q9et35 | mus musculus |
| O6bu93 | debaromyce |
| Q9m3b3 | arabidopsis |
| Q9x0n0 | thermotoga |
| O6csu4 | kluyveromyc |
| Q9xv87 | caenorhabdi |
| Q9fj83 | arabidopsis |
| O45251 | caenorhabdi |
| O6lhf6 | photobacter |
| Cag23274 | photobact |
| Q7nbh6 | mycoplasma |
| O42637 | neutrospora |
| Q7s820 | neutrospora |
| Q7rm66 | plasmodium |
| O63661 | rattus norv |
| Q63661 | giardia lam |
| Q8d6l4 | vibrio vuln |
| Q76nx0 | dictyosteli |
| Aam093326 | dictyosteli |
| O6fj9 | candida gla |
| O8jkv7 | heliobact |
| Q74910 | schizosacch |
| Q97eb5 | clostridium |
| Q8gh21 | dictyosteli |
| Q9bi07 | entamoeba h |
| O60932 | brassica ol |
| O6fk14 | candida gla |
| Q7z5t8 | homo sapien |
| Q8iz06 | homo sapien |
| Q6fk22 | candida gla |
| Q6w4x9 | homo sapien |
| Aa82434 | homo sapi |
| Q8c3k1 | mus musculus |
| Q41771 | kluyveromyc |
| Q7ztml | xenopus lae |
| Q7qy47 | giardia lam |
| Q9ykv7 | human immun |
| Q22378 | caenorhabdi |
| Q7qt2 | giardia lam |
| Q8kmk7 | mycoplasma |
| Q9rh05 | streptomyce |
| Q91000 | gallus gall |
| Q8nfy8 | homo sapien |

RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.,
 RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RL Nature 404:995-999(2000).
 RN [6]
 RN FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
 RP MEDLINE=211170294; PubMed=10973284; DOI=10.1038/79802;
 RX Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [9]
 RN INTERACTIONS WITH TRAF5 AND TRAF6.
 RP MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
 RX Shu H.-B., Johnson H.;
 RA "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia
 CC (T-ALL) by a chromosomal translocation t(4;16)(q26;p13), which
 CC involves TNFSF17 and IL2.
 CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
 CC -----
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 CC -----
 DR EMBL; Z14954; CAA78679.1; -;
 DR EMBL; Z29575; CAA82691.1; -;
 DR EMBL; Z29574; CAA82690.1; -;
 DR EMBL; U95742; AAB67251.1; -;
 DR EMBL; AB052772; BAB60895.1; -;
 DR EMBL; AY509112; AAR84240.1; -;
 DR PIR; S43486; S43486.
 DR PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R=8-46.
 DR Genew; HGNC:11913; TNFRSF17.
 DR MIM; 109545; -;
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 KW 3D-structure; Chromosomal translocation; Immune response;
 KW Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 77 Signal-anchor for type III membrane
 FT protein (Potential).
 FT DOMAIN 78 184 Cytoplasmic (Potential).
 FT REPEAT 7 41 TNFR-Cys.
 FT SITE 3 4 Breakpoint for translocation to form
 FT IL2/TNFSF17 oncogene.
 FT DISULFID 8 21 By similarity.
 FT DISULFID 24 37 By similarity.
 FT DISULFID 28 41 By similarity.
 FT VARIANT 54 54 A -> V.
 FT VARIANT 65 65 FTId=VAR_018755.
 FT I -> V.

RA RESULT 1
 TR17 HUMAN
 ID TR17 HUMAN STANDARD; PRT; 184 AA.
 AC Q02223;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN Name=TNFRSF17; Synonyms=BCMA, BCM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
 RC TISSUE=Lymph node, and Peripheral blood leukocytes;
 RX MEDLINE=93010984; PubMed=1396583;
 RA Laabi Y., Gras M.P., Carbone F., Brouet J.C., Berger R.,
 RA Larsen C.J., Tsapis A.;
 RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
 RT by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
 RL EMBO J. 11:3897-3904(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94218235; PubMed=8165126;
 RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
 RT "The BCMA gene, preferentially expressed during B lymphoid maturation,
 RT is bidirectionally transcribed.";
 RL Nucleic Acids Res. 22:1147-1154(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99425270; PubMed=10493829;
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
 RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
 RA Desliatts Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
 RT "Genome duplications and other features in 12 Mb of DNA sequence from
 RT human chromosome 16p and 16q.";
 RL Genomics 60:295-308(1999).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT THR-153.
 RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
 RA Kawasaki T., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
 RT "Presence of four major haplotypes in human BCMA gene: lack of
 RT association with systemic lupus erythematosus and rheumatoid
 RT arthritis.";
 RL Genes Immun. 2:276-279(2001).
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND
 RP SER-165.
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
 RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
 RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
 RX MEDLINE=20363816; PubMed=10903733;
 RA Hatzoglu A., Roussel J., Bourgade M.-F., Rogier E., Madry C.,
 RA Inoue J.-I., Dovesne O., Tsapis A.;
 RT "TNF receptor family member BCMA (B cell maturation) associates with
 RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
 RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
 RT activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,

FT VARIANT 75 75 /FTid=VAR_018756.
 FT F -> V.
 FT VARIANT 81 81 /FTid=VAR_018757.
 FT S -> N.
 FT VARIANT 153 153 /FTid=VAR_018758.
 FT A -> T.
 FT VARIANT 165 165 /FTid=VAR_012234.
 FT C -> S.
 FT /FTid=VAR_018759.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.4e-81;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEYFDSILLHACIPQCLRCSSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||
 DB 1 MLQMGQCSQNEYFDSILLHACIPQCLRCSSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||

QY 61 GLSLIISLAVFVLMFLRLKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 DB 61 GLSLIISLAVFVLMFLRLKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||

QY 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 DB 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||

QY 181 ISAR 184
 |||||
 DB 181 ISAR 184
 |||||

RESULT 2
 Q6PE46 PRELIMINARY; PRT; 184 AA.

AC Q6PE46
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Tumor necrosis factor receptor superfamily, member 17.
 GN Name=TNFRSP17;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAH58291.1; -.
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

Query Match 99.6%; Score 960; DB 2; Length 184;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAH58291.1; -.
 DR GO; GO:0004872; Fireceptor activity; IEA.
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

Query Match 99.6%; Score 960; DB 2; Length 184;
 Best Local Similarity 99.5%; Pred. No. 3.3e-81;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCSQNEYFDSILLHACIPQCLRCSSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||
 DB 1 MLQMGQCSQNEYFDSILLHACIPQCLRCSSNTPLTCQRYCNASVNSVKGNTNAILWTCL 60
 |||||

QY 61 GLSLIISLAVFVLMFLRLKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||
 DB 61 GLSLIISLAVFVLMFLRLKISSPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
 |||||

QY 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||
 DB 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 |||||

QY 181 ISAR 184
 |||||
 DB 181 ISAR 184
 |||||

RESULT 3
 AAH58291 PRELIMINARY; PRT; 184 AA.

ID AAH58291
 AC AAH58291
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Tumor necrosis factor receptor superfamily, member 17.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC058291; AAH58291.1; -.
 KW Receptor.
 SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;


```
QY 57 WTCLGLSLI--ISLAVFLVFLLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTG 111
DB 81 GLILALTGLVLSVSRWQQRLTASPTDSEGVQOE-----SLENVFPVSSET-- 129
QY 112 EILPRGLEVTVECTEDCIKPKVDSHCPLPAMEGATILVTTKT 161
DB 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATGLGSELVTTKT 170

RESULT 6
Q8R4W8 PRELIMINARY; PRT; 175 AA.
AC Q8R4W8;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE TRAF3 binding protein.
GN Name=Trnf33c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno K., Irie S., Sato T.-A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL83914.1;
DR HSSP; Q96R33; LOQE
DR MGQ; MGI:1919299; Tnfrsf13c.
DR SQ SEQUENCE 175 AA; 18846 MW; B64EFF4B52E93B1 CRC64;

Query Match 12.1%; Score 116.5; DB 2; Length 175;
Best Local Similarity 29.4%; Pred. No. 0.01;
Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

QY 7 QCSQNEYFDSLHACIPCOL-----RCSNTPPLTCQRYCNASVNSVK-----GTNAIL 56
DB 21 QCNQTECFDPLVRNCVSCLEFHTPDGTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80

QY 57 WTCLGLSLI--ISLAVFLVFLLRKIS---SEPLKDFKNTGSGLLGMANIDLEKSRGTG 111
DB 81 GLILALTGLVLSVSRWQQRLTASPTDSEGVQOE-----SLENVFPVSSET-- 129
QY 112 EILPRGLEVTVECTEDCIKPKVDSHCPLPAMEGATILVTTKT 161
DB 130 ----PHASAPTWPLK-EDADSALPR-----HSVPVPATGLGSELVTTKT 170

RESULT 7
TNR6 BOVIN STANDARD; PRT; 323 AA.
AC P51857;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95 antigen).
GN Name=TNFRSF6; Synonyms=AP1, FAS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas. ";
RL DNA Cell Biol. 15:227-234(1996).
CC -1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic
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CC activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
CC SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Contains a death domain involved in the binding of FADD, and maybe to other cytosolic adaptor proteins.
CC -1- SIMILARITY: Contains 1 death domain.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL; U34794; AAC48546.1; -.
CC HSSP; P25445; 1DDF.
CC InterPro; IPR000488; Death.
CC InterPro; IPR011029; DEATH_like.
CC InterPro; IPR008083; Fas_receptor.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00531; Death; 1.
CC Pfam; PF00020; TNFR_C6; 3.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00017; DEATH_DOMAIN; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00050; TNFR_NGFR_2; 2.
CC Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1..36 Potential.
FT CHAIN 17..323 Tumor necrosis factor receptor superfamily member 6.
FT DOMAIN 17..170 Extracellular (Potential).
FT TRANSMEM 171..188 Potential.
FT DOMAIN 189..323 Cytoplasmic (Potential).
FT REPEAT 45..80 TNFR-Cys 1.
FT REPEAT 81..124 TNFR-Cys 2.
FT REPEAT 125..163 TNFR-Cys 3.
FT DOMAIN 238..306 Death.
FT DISULFID 45..56 By similarity.
FT DISULFID 57..70 By similarity.
FT DISULFID 60..79 By similarity.
FT DISULFID 82..98 By similarity.
FT DISULFID 101..116 By similarity.
FT DISULFID 104..124 By similarity.
FT DISULFID 126..140 By similarity.
FT DISULFID 143..154 By similarity.
FT DISULFID 146..162 By similarity.
FT CARBOHYD 38..38 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 115..115 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 323 AA; 36445 MW; 4D8BA90E9E1F4892 CRC64;

Query Match 9.8%; Score 94; DB 1; Length 323;
Best Local Similarity 22.1%; Pred. No. 2.3;
Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;

QY 8 CSQ-NEYFDSLHACIPCOL-----RCSNTPPLTCQRYCNASVNSVK-----T 32
DB 82 CSEGEYTDKSHSDKRCIRCSICDEBHGLEVEQNTCTRTNTRKCRCKSNFFCNPSCEHCN 141
QY 33 PPLTCC-----RYCNASVNSVKGTNA---ILWTCLGLSLIISLAVFLVFLLRKISSEPL 85
DB 142 PCTTCHGIIIEKCTPTSTNTRKCKSRSHANLWAL-----LILLIPVLIIVKVKSRRENK 197
QY 86 KDEFFKNTGSG-----LLGMANIDL-----EKSRTGD--EILPRGLEVTVECTED 130
DB 198 KNYDCNSAASNDGRQLNTDVLGKVPISIAQOMRITVEKFKVKNGM-----EAKIDD 253
```


[1] SEQUENCE FROM N. A.
RP STRAIN=Stock d4-2;
RC
RA Zagulski M., Nowak J. K., Le Mouel A., Nowacki M., Migdalski A.,
EA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
EA Cohen J., Meyer E., Sperling L.;
RT "High coding density on the largest Paramecium tetraurelia somatic
RT chromosome.";
RL Curr. Biol. 0:0-0(2004).
RN [2]

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RC STRAIN=STOCK dg-2;
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR548612; CAH03606.1; --
SQ SEQUENCE 3005 AA; 343421 MW; D8CCG6A247876A5A5 CRC64;

Query Match          9.2%; Score 89; DB 2; Length 3005;
Best Local Similarity 20.3%; Pred. No. 71;
Matches 48; Conservative 26; Mismatches 59; Indels 104; Gaps 13;

Qy 1 MLOWAGQC-SONEYFDSLIHACIPCOLRCSSNTPPLTCQ---RYC----- 41
Db 1177 ILKVGNQCLCKDGYFFSSNTQICTQLDSC-----FTCGSSKCYCLSDCPAFHLQLSNQN 1230
Qy 42 -----NASVTNSVKGTNAILTCGLSLIISLAVFLMLFLRLKISSPFL-----K 86
Db 1231 KCTCDSGYFNTS-TKQCACNITCKECSVS-----QCTCEPMTRYNDR 1275
Qy 87 DEFKNTGSGLLGMANIDLEKSNRTGDBIILPRGLEVTVE-----ECTCEDCTKSKPKV-- 138
Db 1276 DTFK-----CLCKDGFYETIEIKKQCPDWTCKTCVSQSTKCLT 1313
Qy 139 -----DSHCHPFLPAMEE--GATILVTTKTNIDYCKSLPA-----ALSATEIEK 179
Db 1314 CESIHILRSFNNSNKK--FCLDGYFDVVGIEMCQKNDLCKTCQSISTQCLSCVETEQ 1367

RESULT 12
Q97D61
ID Q97D61 PRELIMINARY; PRT; 217 AA.
AC Q97D61

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01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Amino acid ABC transporter, permease component.
DE OrderedLocusNames=CAC3619;
GN Cn
OS Clostridium acetobutylicum.
OC Bacterii; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=12559325; PubMed=11466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton J., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Olud. H. Hitti J., Wolf Y.I.

DAI M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RA *Bacterium Clostridium acetobutylicum*.";
RT J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. (By similarity).
CC -!- SIMILARITY: belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AE007858; AAK81542.1; -.
DR PIR; C97344; C97344.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.


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DR GO: GO:0005903; C:brush border; IDA.
DR GO: GO:0005887; C:integral to plasma membrane; IDA.
DR GO: GO:0005902; C:microvillus; IDA.
DR InterPro: IPR008795; Prominin.
DR Pfam: PF05478; Prominin; 1.
SQ SEQUENCE 823 AA; 92225 MW; 95F01A18DB84EFAC CRC64;

Query Match          9.0%; Score 86.5; DB 2; Length 823;
Best Local Similarity 22.7%; Pred. No. 31;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQCLRCSSNTPTLCQRYCNASVTSVKGTAAILWTCLGLSLIISLAVFVLMFL 77
DB 117 LVGCFPCMCRC-----CNK-CGGEHQKQKQAPCRKCLGLSLVLCILMSIGIY 167

QY 78 RKISSEPLKDFKNTGSLGLGMANIDLEKSTGPD-EIIL---PRGLEYYVEECTCE--- 129
DB 168 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNTKKA 218

QY 130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
DB 219 FSDLDGIGSVLGRKQKPKV-----TPVLEEIKAWATAIKQTKDALQNMSSSLKS 271

QY 173 ---SATEIEKSISA 183
DB 272 LQDAATQTLNTLSS 285

RESULT 16
Q8CDK8 ID Q8CDK8 PRELIMINARY; PRT; 827 AA.
AC Q8CDK8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4931440N24 product:prominin, full insert sequence.
GN Name=Promi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP
RP RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN RP
RP RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN RP
RP RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN RP
RP RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

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RN RP
RP RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Kitsuunai T., Tashiro H., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Katsura M., Nishine T., Harada A.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Ikegami T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Izawa M., Ohara E., Watanabe M.,
RA Fujiwaka S., Inoue K., Togawa Y., Tanaka T., Tanaka T., Hayashizaki Y.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RP
RP RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR DR MGD; MGI:1100886; Promi.
DR GO: GO:0005903; C:brush border; IDA.
DR GO: GO:0005887; C:integral to plasma membrane; IDA.
DR GO: GO:0005902; C:microvillus; IDA.
DR InterPro: IPR008795; Prominin.
DR Pfam: PF05478; Prominin; 1.
SQ SEQUENCE 827 AA; 92714 MW; DBCA5ED2DF401A18 CRC64;

Query Match          9.0%; Score 86.5; DB 2; Length 827;
Best Local Similarity 22.7%; Pred. No. 31;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQCLRCSSNTPTLCQRYCNASVTSVKGTAAILWTCLGLSLIISLAVFVLMFL 77
DB 117 LVGCFPCMCRC-----CNK-CGGEHQKQKQAPCRKCLGLSLVLCILMSIGIY 167

QY 78 RKISSEPLKDFKNTGSLGLGMANIDLEKSTGPD-EIIL---PRGLEYYVEECTCE--- 129
DB 168 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNTKKA 218

QY 130 ----DCIKS-----KPKVDSHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
DB 219 FSDLDGIGSVLGRKQKPKV-----TPVLEEIKAWATAIKQTKDALQNMSSSLKS 271

QY 173 ---SATEIEKSISA 183
DB 272 LQDAATQTLNTLSS 285

RESULT 17
Q8BH12 ID Q8BH12 PRELIMINARY; PRT; 834 AA.
AC Q8BH12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Prominin T1 isoform (Mus musculus adult male testis cDNA, RIKEN full-
DE length enriched library, clone:4932416E19 product:prominin, full
DE insert sequence).
GN Name=Promi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Testis;
 RA Fargues C.A., Hutter W.B., Corbeil D.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The PANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Hayashizaki Y.,
 RA Konno H., Okazaki Y., Muramatsu M., Sugahara Y., Shibata K., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=1076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamaoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Himamoto K., Hizaoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF305215; AK011840.1; -
 DR EMBL; AK030027; BAC26745.1; -
 DR MGD; MGI:1100886; Prom1.
 DR GO; GO:0005903; C:brush border; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0005902; C:microvillus; IDA.
 DR InterPro; IPR008795; Prominin.1.

DR Pfam; PF05478; Prominin; 1.
 SQ SEQUENCE 834 AA; 93444 MW; 5ABA26C80F636B45 CRC64;
 Query Match 9.0%; Score 86.5; DB 2; Length 834;
 Best Local Similarity 22.7%; Pred. No. 32;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
 QY 18 LHACIFCQURCSSNTPLPTCQRYCNASVTVSGTNAITLWTCGLSLIIISLAVFLMFL 77
 DB 117 LVGCFCCMCR-----CNK-CGGEHQONAPCRKCLGLSLVCLLSLGIY 167
 QY 78 RKISSPLKDEFPKNTGSLGGMANIDLEKSRGCD-EILL---PRGLEVTVECTCE---- 129
 DB 168 GFVANQOTTRIRKGTOK-----LAKSNFRDFTLLTETPKQIDYVVEQVTNTKKA 218
 QY 130 -----DCIKS-----KPKVDSHCFPLPAMEGATILVTTK-TNDYCKSLPAAL-- 172
 DB 219 FSLDLDGSGVLGRIKDLKPKV-----TPVLEIKANATAIKQTKDALQNMSSLSKS 271
 QY 173 ---SATEIEKSIISA 183
 DB 272 LQDAATQLNTNLSS 285
 RESULT 18
 Q8R056
 ID Q8R056 PRELIMINARY; PRT; 842 AA.
 AC Q8R056;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Prom1 protein.
 GN Names=Prom1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028286; AAH28286.1; -
 DR MGD; MGI:1100886; Prom1.
 DR GO; GO:0005903; C:brush border; IDA.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0005902; C:microvillus; IDA.
 DR InterPro; IPR008795; Prominin.1.
 DR Pfam; PF05478; Prominin; 1.

SQ SEQUENCE 842 AA; 94478 MW; 734C10D715B5BC92 CRC64;

Query Match 9.0%; Score 86.5; DB 2; Length 842;
Best Local Similarity 22.7%; Pred. No. 32;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQLRCSNTPPLTCQRYCNASVTSVKGNTNAILMTCLGLSLIISLAVFLMFL 77
DB 126 LVGCFPCMCRC-----CNK-CGEGMHQKQKQAPCRRKCLGLSLVLCILMSLGIY 176

QY 78 RKISSEPLKDFKNTGSGLLGMANIDLEKSTGD-EIIL----PRGLETVVECTCE---- 129
DB 177 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNKKA 227

QY 130 -----DCIKS-----KPKVDSHCFPLPAMEEGATILVTK-TNDYCKSLPAAL-- 172
DB 228 FSDLGIGSVLGRKIDQLKPKV-----TPVLEIKAMATAIKQTKDALQNMSSLSKS 280

QY 173 ---SATEIEKSISA 183
DB 281 LQDAATQLTNLSS 294

RESULT 19

PML1 MOUSE

ID PML1 MOUSE STANDARD; PRT; 867 AA.

AC O54950; O35408;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Prominin 1 precursor (prominin-like protein 1) (Antigen AC133 homolog).

GN Name=Prom1; Synonyms=Prom11, Prom;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Miraglia S., Godfrey W., Buck D.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=98024147; PubMed=9356465;

RA Weigmann A., Corbeil D., Hellwig A., Huttner W.B.;

RT "Prominin, a novel microvilli-specific polytopic membrane protein of the apical surface of epithelial cells, is targeted to plasmalemma protrusions of non-epithelial cells.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430(1997).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: In the embryo, expressed on the apical side of neuroepithelial cells and of other epithelia such as lung buds, gut and ureter buds. In the adult, expressed at the apical side of the kidney tubules and of the ependymal layer of the brain. Not expressed in gut, liver, lung, pituitary, adrenal, heart or spleen.

CC -1- SIMILARITY: Belongs to the prominin family.

CC

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CC

DR EMBL; AF039663; AAB96916.1; -

DR EMBL; AF026269; AAB86715.1; -

DR PIR; T08881; T08881.

DR MGI; MGI:1100886; Prom1.

DR GO; GO:0005903; C:brush border; IDA.

DR GO; GO:0005887; C:integral to plasma membrane; IDA.

DR GO; GO:0005902; C:microvillus; IDA.

DR InterPro; IPR008795; Prominin.

DR Pfam; PF05478; Prominin; 1.

KW Glycoprotein; Signal; Transmembrane.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 867 Prominin 1.

FT DOMAIN 20 107 Extracellular (Potential).

FT TRANSMEM 108 128 Potential.

FT DOMAIN 129 158 Cytoplasmic (Potential).

FT TRANSMEM 159 179 Potential.

FT DOMAIN 180 434 Extracellular (Potential).

FT TRANSMEM 435 455 Potential.

FT DOMAIN 456 487 Cytoplasmic (Potential).

FT TRANSMEM 488 508 Extracellular (Potential).

FT DOMAIN 509 794 Potential.

FT TRANSMEM 795 815 Potential.

FT DOMAIN 816 867 Cytoplasmic (Potential).

FT CARBOHYD 273 273 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 291 291 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 332 332 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 374 374 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 415 415 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 554 554 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 581 581 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 732 732 N-linked (GlcNAc. .) (Potential).

FT CONFLICT 64 64 S -> N (in Ref. 2).

FT CONFLICT 84 84 K -> N (in Ref. 2).

FT CONFLICT 94 102 Missing (in Ref. 2).

FT CONFLICT 668 668 P -> L (in Ref. 2).

FT CONFLICT 844 844 G -> D (in Ref. 2).

SQ SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;

Query Match 9.0%; Score 86.5; DB 1; Length 867;
Best Local Similarity 22.7%; Pred. No. 33;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPQLRCSNTPPLTCQRYCNASVTSVKGNTNAILMTCLGLSLIISLAVFLMFL 77
DB 126 LVGCFPCMCRC-----CNK-CGEGMHQKQKQAPCRRKCLGLSLVLCILMSLGIY 176

QY 78 RKISSEPLKDFKNTGSGLLGMANIDLEKSTGD-EIIL----PRGLETVVECTCE---- 129
DB 177 GFVANQQTTRIKGTQK-----LAKSNFRDFQTLTETPKQIDYVVEQYTNKKA 227

QY 130 -----DCIKS-----KPKVDSHCFPLPAMEEGATILVTK-TNDYCKSLPAAL-- 172
DB 228 FSDLGIGSVLGRKIDQLKPKV-----TPVLEIKAMATAIKQTKDALQNMSSLSKS 280

QY 173 ---SATEIEKSISA 183
DB 281 LQDAATQLTNLSS 294

RESULT 20

Q6CCL1

ID Q6CCL1 PRELIMINARY; PRT; 1309 AA.

AC Q6CCL1;

DT 01-OCT-2004 (TrEMBLrel. 28, Created)

DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Similar to sp|P08640|Saccharomyces cerevisiae YIR019c STAI extracellular alpha-1.

GN ORFNames=VALI0C08473g;

OS Yarrowia lipolytica (Candida lipolytica).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Dipodascaceae; Yarrowia.

OX NCBI_TaxID=4952;

[1]

RN SEQUENCE FROM N.A.

RC STRAIN=CLIB99;

RG GENOLEVURES;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neveuglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anchouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
 RA Kerrast A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicraud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Weyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382129; CAG81904.1; -;
 SQ SEQUENCE 1309 AA; 137079 MW; 7D2E2927115D6CC2 CRC64;

Query Match 8.9%; Score 86; DB 2; Length 1309;
 Best Local Similarity 24.0%; Pred. No. 56;
 Matches 52; Conservative 17; Mismatches 78; Indels 70; Gaps 11;

QY 21 CIPCLRCSSNPPLTCQRYCNAS-----VTNSVKGNTNAILWT--CLGLSLIISLA 69
 DB 813 CLETVVASISGPTTIVINNICTSAPVPCLEVTASVSGSTIVINDICKTVDPICITTE 872

QY 70 VFVLMFLLRKISSEP---LKDFPKNTGSGLLGMANIDLE---KSRGTD-----E 112
 DB 873 VVT-----VSGTPATMTKDVQCTTADPCLETAIVTLGTPATVTKDICTSADPCVETE 925

QY 113 ILPRGLETVBECTCEDCKSPKVD-----SDHCFPLPAMEEGAT 154
 DB 926 VTVVSGTSTV---TKNSCITSTPVADPCVVTETISSGITEVITRDICTPAPTVPVVTST 982

QY 155 ILV---TTKT-----NDYCKSLPA-----ALSATEI 177
 DB 983 VTVPATITKTITVCEBEVCTTIPVTLTALVLSSTEI 1019

RESULT 21
 QY1X8
 ID QY1X8 PRELIMINARY; PRT; 1193 AA.
 AC QY1X8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Protein tyrosine kinase.
 GN Name=EFTK178;
 OS Ephydatia fluviatilis.
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haploclerida; Spongillidae; Ephydatia.
 OX NCBI_TaxID=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99246375; PubMed=10229568;
 RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
 RA Miyata T.;
 RT "Extensive gene duplication in the early evolution of animals before
 RT the parazoan-eumetazoan split demonstrated by G proteins and protein
 RT tyrosine kinases from sponge and hydra.";
 RL J. Mol. Evol. 48:646-653(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21601119; PubMed=11738833;
 RA Suga H., Katoh K., Miyata T.;
 RT "Sponge homologs of vertebrate protein tyrosine kinases and frequent
 RT domain shufflings in the early evolution of animals before the
 RT parazoan-eumetazoan split.";

RL Gene 280:195-201(2001).
 DR EMBL; AB008570; BAA81724.2; -;
 DR HSSP; P08069; 1JQH.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
 DR InterPro; IPR000494; EGFR_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00261; FU; 6.
 DR SMART; SM00219; TyRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00552; TNFR_NGFR_1; UNKNOWN 1.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1193 AA; 128169 MW; 009E4AC9BC12DF60 CRC64;

Query Match 8.9%; Score 85.5; DB 2; Length 1193;
 Best Local Similarity 22.3%; Pred. No. 57;
 Matches 37; Conservative 28; Mismatches 56; Indels 45; Gaps 8;

QY 2 LQWAGCQSNQYFDSLHACIPQLRCSNTTP-----LTCQRYCNASVTNSVKGNTNAIL 56
 DB 715 LCVSGCSNDTEYQDAALN-CLPCAAGCICGSGPSISQCLTCA--SGSCTTTDVQSSGGII 771

QY 57 WTCLGLSLIISLA---VFVLMFLLRKISSEPKDFKNTGSGLLGMANIDLEKSRGTGDEI 113
 DB 772 GIVFGSIVVIFLATSIVLILFIVRYEYHKVFNKRTQSTA---MCYSN-----GNET 820

QY 114 ILPRGLETVBECTCEDCKSPKVDSDH-----CPPLPAMEEGATI 155
 DB 821 LRP-----PKLPPDATRLIITPETALEQCVL 847

RESULT 22
 Q8RWV7
 ID Q8RWV7 PRELIMINARY; PRT; 938 AA.
 AC Q8RWV7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein At3g48195.
 GN Name=At3g48195;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY091078; AAM13898.1; -.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001683; PX.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS0195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 938 AA; 103602 MW; 3E78395D65D75C95 CRC64;

Query Match      8.7%; Score 83.5; DB 2; Length 938;
Best Local Similarity 29.4%; Pred. No. 68;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Qy 38 QRYCNASVTNSVKGNTNAILWTCLGLSLIISLAVFLMFLRLKTSSEPLKD-EFKN--TGS 94
Db 29 ERYCSA---NSALGTFSM---C-----SSTGPFQDSEFENSLGP 62

Qy 95 GLGGMANIDLEKSRGTGDEIILPRGLETVTECTCECIKSKP-----KVDSHCFPLPAM 149
Db 63 SLVKLSLDM--SRLGD-----RGIHFDEGGSCNGRSSSAPGLNTGNVNDMCGDL--M 113

Qy 150 EEGATI 155
Db 114 DGGATI 119

RESULT 23
Q9STR8 PRELIMINARY; PRT; 1998 AA.
AC Q9STR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T24C20_80.
GN Names=T24C20_80;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosidia II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choise N., Robert C., Brottier P., Winck P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
RA Lencke K., Mayer K.F.X., Queirer F., Salanoubat M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096856; CAB51067.1; -.
DR PIR; T13009; T13009.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS0195; PX; 1.
KW Hypothetical protein.
SQ SEQUENCE 1998 AA; 223512 MW; 8B3D6A03CD248F55 CRC64;

Query Match      8.7%; Score 83.5; DB 2; Length 1998;
Best Local Similarity 29.4%; Pred. No. 1.5e+02;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

Qy 38 QRYCNASVTNSVKGNTNAILWTCLGLSLIISLAVFLMFLRLKTSSEPLKD-EFKN--TGS 94
Db 1089 ERYCSA---NSALGTFSM---C-----SSTGPFQDSEFENSLGP 1122

Qy 95 GLGGMANIDLEKSRGTGDEIILPRGLETVTECTCECIKSKP-----KVDSHCFPLPAM 149
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Db 1123 SLVKLSLDM--SRLGD-----RGIHFDEGGSCNGRSSSAPGLNTGNVNDMCGDL--M 1173
Qy 150 EEGATI 155
Db 1174 DGGATI 1179

RESULT 24
Q8C6R5 PRELIMINARY; PRT; 449 AA.
AC Q8C6R5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-
DE length enriched library, clone:E230011L17 product:protein tyrosine
DE kinase 2 beta, full insert sequence. (fragment).
GN Names=Ptk2b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20499374; PubMed=11042159;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kusunagi T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20530913; PubMed=11076861;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichou H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK054002; BAC35615.1; -.
DR MGD; MGI:104908; Ptk2b.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; IDA.
DR GO; GO:0004672; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011009; Kinase_like.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS50057; FERM_3; 1.
KW KINASE.
FT NON TER 449 449
SQ SEQUENCE 449 AA; 51577 MW; D3565BCBA7D32B84 CRC64;

Query Match 8.6%; Score 83; DB 2; Length 449;
Best Local Similarity 26.9%; Pred. No. 35;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEILPRGLTYVECTCEDCIKSPKV 138
Db 249 KPFNT---LAGFANIDQETVRCLEIQGNWITVDLVIGPKGIQLTSQDTKPTCLAEFKQI 305

QY 139 DSDHCPLPAME-----EGATILVTTKND-----YCK 166
Db 306 KSIKRLPLEETQAVLQIGIEGAPQSLSIKTSSLAENMADLDGYCR 353

RESULT 25
Q8C9L4 PRELIMINARY; PRT; 474 AA.
AC Q8C9L4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630043J01 product:protein tyrosine kinase 2 beta, full
DE insert sequence.
GN Names=Ptk2b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

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RL Nature 420:563-573(2002).
RN [4]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Iehli Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuura S.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
SQ SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
RC STRAIN=C57BL/6J; Arakawa T., Bono H., Carninci P.,
RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
RA Hayashida K., Hayatsu N., Hiramoto K., Kondo S., Kouda M., Koya S.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Konno H., Kouda M., Koya S.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichou H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK041878; BAC31090.1; -.
DR MGD; MGI:104908; Ptk2b.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; IDA.
DR GO; GO:0004672; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011009; Kinase_like.
DR SMART; SM00295; B41; 1.
DR PROSITE; PS50057; FERM_3; 1.
KW Kinase.
SQ SEQUENCE 474 AA; 54201 MW; A1A83BCB191B55FB CRC64;

Query Match 8.6%; Score 83; DB 2; Length 474;
Best Local Similarity 26.9%; Pred. No. 37;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEILPRGLTYVECTCEDCIKSPKV 138
Db 249 KPFNT---LAGFANIDQETVRCLEIQGNWITVDLVIGPKGIQLTSQDTKPTCLAEFKQI 305

QY 139 DSDHCPLPAME-----EGATILVTTKND-----YCK 166
Db 306 KSIKRLPLEETQAVLQIGIEGAPQSLSIKTSSLAENMADLDGYCR 353

RESULT 26
Q7RAAS PRELIMINARY; PRT; 164 AA.
ID Q7RAAS;
AC Q7RAAS;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DHHC zinc finger domain, putative.

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GN Name=PY06597;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Koolij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shaillon S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser F.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002253; EXA18941.1; -.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro; IPR001594; Znf.DHHC.
DR Pfam; PF01529; znf-DHHC; I.
DR ProDom; PD003041; Znf.DHHC; 1.
DR PROSITE; PS00216; Znf.DHHC; 1.
DR SEQUENCE 164 AA; 19593 MW; CPDFF8E6B6B90FF1 CRC64;

Query Match 8.6%; Score 82.5; DB 2; Length 164;
Best Local Similarity 31.2%; Pred. No. 14;
Matches 34; Conservative 12; Mismatches 34; Indels 29; Gaps 7;

QY 47 NSVKGTTNAILWTCIGLSLIISLAVFLVLMFLRKISS-----EPLKDE--FKNTGSGLL 97
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 NKMKINLFIF-CQGIKILIFHFLMLFLINILSVTPPGFIPNTEWVFKDFGEN-- 63
| : : : : : : : : : : : : : : : : : : : : : : : :

QY 98 GMANID---LEKSTGDEIILPRGLETVVECTCECIKSKPKVDSDHC 143
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 NSNNIDYLLLEKKTG-----ERRFCCKCKYKPD-RAHHC 98
| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 27
Q6CCL7 PRELIMINARY; PRT; 1142 AA.
AC Q6CCL7;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=ALI0C083499;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG GNOLFEVRES;
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boelsame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,

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RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382129; CAG81898.1; -.
SQ SEQUENCE 1142 AA; 121017 MW; 11D636A6296F1912 CRC64;

Query Match 8.6%; Score 82.5; DB 2; Length 1142;
Best Local Similarity 25.6%; Pred. No. 1e+02;
Matches 46; Conservative 23; Mismatches 72; Indels 39; Gaps 10;

QY 29 SSTPTTCORYCNASVTNSVKGTTNAILWT--CLGLSLIISLA-VFVLMFLRKISSEPL 85
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 778 SSNIAP-TTPNCPNVVESATISGTPTVTSDFCQSSDSVSTAPISSAPISSDPF 836
| : : : : : : : : : : : : : : : : : : : : : : : :

QY 86 KDEFKNTGSGLLGMANIDLEKSTGD-----EILPRGLETVV--EBC----- 126
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 TVEHPVTSGTSPSVLTLDLSLTISNPCIETEVAVSGVEFTVKNCPSAPVSLVPSS 896
| : : : : : : : : : : : : : : : : : : : : : : : :

QY 127 ---TCEDCIKSKPK---VSDHCFLPAMBEAGATILV-TTKT-----NDYCKSLPALSA 174
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 897 TPAACVETITVSGKSVINKEEC-----NVTSTVTLAPITKTITHCDNESCTAIPVTLA 952
| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 28
O97491 PRELIMINARY; PRT; 327 AA.
ID O97491;
AC O97491;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas protein.
GN Names=Fas;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocyte;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1; -.
DR HSP; P25445; 1DDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;

Query Match 8.5%; Score 82; DB 2; Length 327;
Best Local Similarity 23.0%; Pred. No. 31;
Matches 54; Conservative 25; Mismatches 68; Indels 88; Gaps 15;

```

QY 8 CSQ-NEVFDLSLHA-CIPCOL-----RCSSN-----T 32
DB 84 CSENEYTDKSHSDKIRCSCDEEHGLEVEHNECTRTONTKCRCKSNFFCNSPCEHCN 143
QY 33 PPLTCQ---RYCNASVTNSVKG---TNAIWTCLGLSLIISLAVFLMLRK----- 79
DB 144 PCTTCEHGIIETKPTNTSKCRSRHTNS-LWALLILLILLIILYKVRRRNRKK 202
QY 80 ---ISSEPLKDEFKNTGSGLLGMANIDLEKSRGTG-----DEIILPRGLETVVEEC 126
DB 203 NGNCVSAASDEGRQ-----LNLTDVLDGKYIPSIABLMKITEKFEVRKNGM-----EEA 253
QY 127 TCSDCTKSQKPVSDHCPPLPAMEGATIL-----VTTKNDYV---KSLPAALS 173
DB 254 KIDDIIMH-----DNLH---ETAQKQVLLRKRYQSHGKNAYCTLTKNLPKALA 299
RESULT 29
Q8C2G0 PRELIMINARY; PRT; 967 AA.
AC Q8C2G0
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:B430023005 product:protein tyrosine kinase 2 beta, full insert sequence.
DE Name=Ptk2b;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX The FANTOM Consortium;
RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akizawa J., Nishi K., Kiteunai T., Tachiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., RA Fukuchi S., Furuno M., Hanagaki T., Hara A., Hashizume W., RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK088696; BAC40510.1; -
DR HSSP; Q05397; 1K04.
DR MGD; MGI:104908; Ptk2b.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; P:protein kinase activity; IDA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR005189; Focal AT.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF03623; Focal AT; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00057; FERM 3; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 967 AA; 111131 MW; D65A8C3847BA62F CRC64;
Query Match 8.5%; Score 82; DB 2; Length 967;
Best Local Similarity 26.9%; Pred.No. 97;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
QY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLETVVEECTCDCKSPKV 138
DB 249 KFNT---LAGFANIDQETVRCLEIQQWITVDLVIGPKGIRQLTSDTKPTCLAEPKQI 305
QY 139 DSDHCPPLPAME-----EGATILVTTKND-----YCK 166
DB 306 RSTRCPLPTEOAVLQGLGEGAPQSLSIKTSSLAEEANMADLIDGYCR 353
RESULT 30
FAK2_MOUSE
ID FAK2_MOUSE STANDARD; PRT; 1009 AA.
AC Q9QVF9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase 2) (PAK2 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related adhesion focal tyrosine kinase).
DE Name=Ptk2b; Synonyms=FAK2, PYK2, Raftek;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RA "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain.";
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [2]
 RP PTNS1 BINDING.
 RX MEDLINE=99401000; PubMed=10469599;
 RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
 RA Schraven B., Neel B.G.;
 RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
 RT multi-protein complexes in macrophages.";
 RL Curr. Biol. 9:927-930(1999).
 RN [3]
 RP PHOSPHORYLATION SITES TYR-402; TYR-580 AND TYR-881.
 RX MEDLINE=21313779; PubMed=11420674; DOI=10.1038/sj/onc/1204359;
 RA Nakamura K., Yano H., Schaefer E., Sabe H.;
 RT "Different modes and qualities of tyrosine phosphorylation of Pak and
 RT Pyk2 during epithelial-mesenchymal transdifferentiation and cell
 RT migration: analysis of specific phosphorylation events using site-
 RT directed antibodies.";
 RL Oncogene 20:2626-2635(2001).
 RN [4]
 RP PHOSPHORYLATION SITE TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; PubMed=11493697; DOI=10.1073/pnas.171269898;
 RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Binds DDBP2 (By similarity). Interacts with Crk-
 CC associated substrate (Cas), PTNS1, Nephrocystin and OPHN1L.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-association of the kinase.
 CC -1- PTM: Phosphorylated on tyrosine residues in response to various
 CC stimuli that elevate the intracellular calcium concentration, as
 CC well as by PKC activation. Recruitment by Nephrocystin to cell
 CC matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 CC HSP; Q05397; IK04.
 DR IntAct; Q9QVP9; -.
 DR MGD; MGI:104908; Ptk2b.
 DR InterPro; IPR000299; Band 4.1.
 DR InterPro; IPR009065; FERM¹
 DR InterPro; IPR005189; Focal AT.
 DR InterPro; IPR011009; Kinase¹-like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr.pkinase.
 DR InterPro; IPR008266; Tyr.pkinase_AS.
 DR Pfam; PF03623; Focal AT; 1.
 DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; TykKc; 1.
 DR PROSITE; PS00660; FERM 1; FALSE NEG.
 DR PROSITE; PS00661; FERM 2; FALSE NEG.
 DR PROSITE; PS00057; FERM 3; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Phosphorylation; transferase; Tyrosine-protein kinase.
 FT DOMAIN 39 359 FERM.
 FT DOMAIN 425 683 Protein kinase.
 FT NP_BIND 431 439 ATP (By similarity).
 FT BINDING 457 457 ATP (By similarity).
 FT ACT_SITE 549 549 Proton acceptor (By similarity).
 FT DOMAIN 701 767 Pro-rich.
 FT DOMAIN 831 869 Pro-rich.
 FT DOMAIN 868 1009 Focal adhesion targeting (FAT).
 FT MOD_RES 402 402 Phosphotyrosine.
 FT MOD_RES 579 579 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 580 580 Phosphotyrosine.
 FT MOD_RES 881 881 Phosphotyrosine.
 SQ SEQUENCE 1009 AA; 115821 MW; 963959FF56DF9605 CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 1e+02;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
 OY 88 EFKNTGSGLLGMANIDLEKSR-----TGDEILPRGLEVTVECTCDCKSPKV 138
 DB 249 KPFNT--LAGFANIDQETVRCLEIQGMNITVDLVIGPKGIRQLTSQDKPTCLAEFKOI 305
 OY 139 DSDHCPLPAME-----EGATILVTXTND-----YCK 166
 DB 306 RSIRCLPLEBTOAQLQGLGEGAPQSLSIKTSLSLAENMADLIDGYCR 353
 RESULT 31
 FAK2_RAT
 ID_FAK2_RAT STANDARD; PRT; 1009 AA.
 AC P70600; O88489; Q63201;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 DE 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 DE beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
 GN Names=Ptk2b; Synonyms=Fak2; Pyk2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE=Liver epithelium;
 RX MEDLINE=97094711; PubMed=8939945;
 RA Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 RA Wilms M., Anderregg R.J., Graves L.M., Earp H.S.;
 RT "Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 RT protein kinase activation.";
 RL J. Biol. Chem. 271:29993-29998(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95403356; PubMed=7673154;
 RA Sasaki H., Nagura K., Ishino M., Tobitoka H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 RT protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).

[3]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
DOMAIN.
TISSUE=Hippocampus;
MEDLINE=98311659; PubMed=9645946;
Xiong W.-C., Macklem M., Parsons J.T.;
"Expression and characterization of splice variants of PK2, a focal
adhesion kinase-related protein.";
J. Cell Sci. 111:1981-1991(1998).
CC -|- FUNCTION: Involved in calcium induced regulation of ion channel
and activation of the map kinase signaling pathway. May represent
an important signaling intermediate between neuropeptide activated
receptors or neurotransmitters that increase calcium flux and the
downstream signals that regulate neuronal activity. Interacts with
the SH2 domain of Grb2. May phosphorylate the voltage-gated
potassium channel protein Kv1.2. Its activation is highly
correlated with the stimulation of c-Jun N-terminal kinase
activity.
CC -|- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -|- SUBUNIT: Interacts with PTPNS1 and DDEF2 (By similarity). Isoform
1, but not isoform 2, interacts with Crk-associated substrate
(Cas), Nephrocystin and OPHN1L.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
induces the membrane-association of the kinase (By similarity).
CC Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P70600-1; Sequence=Displayed;
CC Name=2; Synonyms=PRNK;
CC IsoId=P70600-2; Sequence=VSP_004982, VSP_004983;
CC Name=3; Synonyms=PYK2a;
CC IsoId=P70600-3; Sequence=VSP_004984;
CC -|- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
in the spleen and other tissues, whereas isoforms 2 and 3 are
expressed in the spleen and brain (highest in cerebellum).
CC -|- PTM: Phosphorylated on tyrosine residues in response to various
stimuli that elevate the intracellular calcium concentration, as
well as by PKC activation. Recruitment by Nephrocystin to cell
matrix adhesions initiates Tyr-402 phosphorylation (By
similarity). In monocytes, adherence to substrata is required for
tyrosine phosphorylation and kinase activation. Angiotensin II,
thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
autophosphorylation and increase kinase activity.
CC -|- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
subfamily.
CC -|- SIMILARITY: Contains 1 FERM domain.

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or send an email to license@isb-sib.ch).

EMBL; U69109; AAC52895.1; -;
EMBL; D45854; BAA0290.1; -;
EMBL; AF063890; AAC28340.1; -;
FIR; A57434; A57434.
DR HSSP; Q05397; 1K04.
DR RGD; 628758; Ptk2b.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR009085; FERM.
DR InterPro; IPR005189; Focal_AT.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF03623; Focal_AT; 1.
DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS0057; FERM_3; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_TYR; 1.
KW Alternative splicing; ATP-binding; Direct protein sequencing;
KW Phosphorylation; Transferase; Tyrosine-protein kinase.
FT DOMAIN 39 359
FT DOMAIN 425 683 Protein kinase.
FT NP_BIND 431 439 ATP (By similarity).
FT BINDING 457 457 ATP (By similarity).
FT ACT_SITE 549 549 Proton acceptor (By similarity).
FT DOMAIN 701 767 Pro-rich.
FT DOMAIN 831 869 Pro-rich.
FT DOMAIN 868 1009 Focal adhesion targeting (FAT).
FT MOD_RES 402 402 Phosphotyrosine (By similarity).
FT MOD_RES 579 579 Phosphotyrosine (by autocatalysis) (By
similarity).
FT MOD_RES 580 580 Phosphotyrosine (By similarity).
FT MOD_RES 881 881 Phosphotyrosine (By similarity).
FT VARSPPLIC 1 771 Missing (in isoform 2).
FT VARSPPLIC 772 780 NVPKRHSR -> MGLIVLSQ (in isoform 2).
FT FTID=VSP_004982.
FT VARSPPLIC 739 780 Missing (in isoform 3).
FT FTID=VSP_004984.
FT CONFLICT 205 205 E -> A (in Ref. 2).
FT CONFLICT 807 807 V -> F (in Ref. 3).
SQ SEQUENCE 1009 AA; 115784 MW; D435A475BCA49E9B CRC64;

Query Match 8.5%; Score 82; DB 1; Length 1009;
Best Local Similarity 26.9%; Pred. No. 1e+02;
Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGILGMANIDLEKSR-----TGDEILPRGLVTECTEDCIKSKPKV 138
Db 249 KFEFT---LAGFANIDQETRYRELIGQWITVDLVIGPKGIQLTSQDKTPTCLAEFKQI 305
QY 139 DSDHCPLPAME-----EGATILVTYKND-----YCK 166
Db 306 RSIRCLPLEETQVLQLGIEGAPQSLSIKTSLSLAENMADLIDGYCR 353

RESULT 32
Q8VEV6 PRELIMINARY; PRT; 314 AA.
AC Q8VEV6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Olfactory receptor MOR202-36 (Olfactory receptor Olfr1475).
GN Name=Olfr1475;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21864068; PubMed=11875048;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory

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receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX MEDLINE=22974002; PubMed=14611657;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels.";
RL Genome Biol. 4:R71-R71(2003).
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
REMBL; AY073792; AAL61455.1; -
DR EMBL; AY318694; AAP71836.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00245; OLFACRORXR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR SMART; SM00639; PSA; 26.
KW Receptor.
SQ SEQUENCE 314 AA; 34996 MW; 9C7B11A5917EA632 CRC64;

Query Match 8.5%; Score 81.5; DB 2; Length 314;
Best Local Similarity 30.4%; Pred. No. 33;
Matches 31; Conservative 16; Mismatches 40; Indels 15; Gaps 6;

QY 8 CSQNEYFDSLHACIP-CQLRCSSNT-----PPLTCQRYCNASVTNSVKGTNAILWT 58
DB 146 CYMGIIQSIHVALACFLSCNSNVNHFCDIPPL-LDISCDYTNIEI--TVLILGT 202

QY 59 CLG-LSLIIISLAVFLVMP--LLRKISSEPLKDFKNTGSLGL 97
DB 203 CDGILTLVILNTVLLIFIALIRMSAEAKAFSTCASHLI 244

RESULT 33
Q94711 ID Q94711 PRELIMINARY; PRT; 2233 AA.
AC Q94711; 1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 51C surface protein.
OS Paramacium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramacium.
OC NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92106337; PubMed=1762150;
RA Nielsen E., You Y., Forney J.;
RT "Cysteine residue periodicity is a conserved structural feature of
variable surface proteins from Paramacium tetraurelia.";
RL J. Mol. Biol. 222:835-841(1991).
DR EMBL; M65164; AAA61740.1; -
DR PIR; T28669; T28669.
DR InterPro; IPR002895; Paramacium SA.
DR Pfam; PF01508; Paramacium SA; 25.
DR SMART; SM00639; PSA; 26.
SQ SEQUENCE 2233 AA; 237076 MW; C064FE0AF7BB873B CRC64;

Query Match 8.4%; Score 81; DB 2; Length 595;
Best Local Similarity 24.5%; Pred. No. 72;
Matches 39; Conservative 27; Mismatches 27; Indels 49; Gaps 10;

QY 6 GQCQNEYFDSLHACIPCOLRCSSNTPLTCQRYCNA-SVTNSVKGTNAILWTCLGLSL 64
DB 520 GSCYQKQ-----CSAASQDNTHAQCOEYLPACTLSNTKKG-----CIDLPL 561
QY 65 IISLAVFLVFLRKISSEPLKDFKNTGSLGLMANIDL-----EKSRTGDEILLPRGLE 120
DB 562 TCSA-----LVKENCCELKANREK---CGWTGSTCVDIVCTTAPTAKTDD-----D 603
QY 121 YTVVEECTC---EDCTKSKPKVDSHCFPLPAMEEGATI-----LVTTKTN 162
DB 604 YTVELCEAYKPSNSCV---PNGTKGCMELAAKCESRTIKEQCQDVAGTKTN 651

RESULT 34
Q39191 ID Q39191 PRELIMINARY; PRT; 595 AA.
AC Q39191; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine threonine kinase.
DE Name:pro25;
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=93066369; PubMed=1438303;
RA Smith T.A., Kohorn B.D.;
RT "An Arabidopsis serine threonine kinase homologue with an EGF repeat
selected in yeast for its specificity for a thylakoid membrane
protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10989-10992(1992).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L04999; AAA32844.1; -
DR HSSP; P01130; 1H28.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF07645; EGF CA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS50026; EGF 3; 2.
DR PROSITE; PS01187; EGF_CA; UNKNOWN 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; EGF-like domain; Kinase; Serine/threonine-protein kinase;
Transferrase.
SQ SEQUENCE 595 AA; 65898 MW; 7B58FCA565E0641 CRC64;

Query Match 8.4%; Score 81; DB 2; Length 595;
Best Local Similarity 24.5%; Pred. No. 72;
Matches 39; Conservative 27; Mismatches 27; Indels 49; Gaps 10;

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OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Science 287:2185-2195(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupu J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.I., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 [5]
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A.
 RP FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003716; AN13739.1; -;
 DR FLYBase; FBgn0051262; CG31262.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001734; Na/solut_sympot.
 DR PROSITE; PS0283; NA SOLUT_SYMP 3; 1.
 SQ SEQUENCE 487 AA; 53156 MW; 454B1312B8CC2C9C CRC64;
 Query Match 8.4%; Score 80.5; DB 2; Length 487;
 Best Local Similarity 23.7%; Pred. No. 65;
 Matches 42; Conservative 28; Mismatches 60; Indels 47; Gaps 8;
 QY 48 SVKGTNAILWTCLGLSLIISLAVFVLMFLLR-----KISSEPLKDEF----- 89
 Db 311 SERQSILIKTCI---IFQILAFILVFLLOHLRGILSVCSISSITAGTSFGVFTLGLML 367
 QY 90 ---KNT-GSGLIGMANIDLEK-SRTGDEILPRG-----LEYVTECTCEDCIKSKPKV 138
 Db 368 FPNANTIGTAGVGLSVLLAGWISFGSIAAASQGLKSGMLPVSVEKCVGNVTLPEDPWV 427
 QY 139 DSPHCPL-----PMEEGATILVTTKNDYCKSLPAALSALETEKSI 181
 Db 428 DQDQVFLYRLSVHWVSPIGWTVAVGVGLVSLITKPAD-IKTLHAELISPVHRSV 483

RESULT 38
 ID 081820 PRELIMINARY; PRT; 735 AA.
 AC 081820;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Wall-associated kinase 1 (Hypothetical protein Atlg21250).
 GN Name=waki; Synonyms=Atlg21250;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99308512; PubMed=10380805;
 RA He Z.H., Cheeseman I., He D., Kohorn B.D.;
 RT "A cluster of five cell wall associated receptor kinase genes, waki-5,
 RT are expressed in specific organs of Arabidopsis."
 RL Plant Mol. Biol. 39:1189-1196(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,

RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AJ006966; CA008794.1; -
DR EMBL: AY039917; AK64021.1; -
DR EMBL: BT001967; AA071966.1; -
DR HSSP: P01130; IZH8.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0005509; P:calcium ion binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000152; Asx hydroxyl_S.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF07645; EGF_CA; 1.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00179; EGF_CA; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 2.
DR PROSITE: PS01187; EGF_CA; UNKNOWN 1.
DR PROSITE: PS00031; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; EGF-like domain; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 735 AA; 81210 MW; AAD41A28296093B6 CRC64;

Query Match 8.3%; Score 80; DB 2; Length 735;
Best Local Similarity 24.2%; Pred. No. 1.1e+02;
Matches 39; Conservative 27; Mismatches 49; Indels 46; Gaps 10;

QY 8 CSNEYFDSLHACIPQ-----LRCSN-----TPLTQCR-----YQNA-----SV 45
DB 264 CRNCEGFGNPNYSAGQDVNCTSTIRHNCSDPKTRNKVGFGYCKQSGYLDIT 323
QY 46 TNSVK-----GTNAITWCLGLSLIISLAVFLMLKISSPLKDE-FKNTGSGLL-- 97
DB 324 TMSCKRKFATWITLLVTTIGF-LVILGVACIQQRMKHLKDTKLRQEPQNGGGLTQ 382
QY 98 -----GNANID-----LEKSRG--DEIILPRGLETVV 123
DB 383 RLSGAGPSNVVDVIFTEGDKMKATNGVAESRIILGQGGQGV 423

RESULT 39
Q8KLY1
ID Q8KLY1 PRELIMINARY; PRT; 153 AA.
AC Q8KLY1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A15101;
RX MEDLINE=22787088; PubMed=12904565;
RA Desnoes N., Lin M., Guo X., Ma L., Carreno-Lopez R., Elmerich C.;
RT "Nitrogen fixation genetics and regulation in a Pseudomonas stutzeri
strain associated with rice.";
RL Microbiology 149:2251-2262(2003).

DR EMBL: AJ297529; CAD44480.1; -
DR GO: GO:001846; F:carbon-sulfur lyase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR006913; GFA.
DR Pfam: PF04828; DUF636; 1.
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17188 MW; 0C849770A6EEA7C7 CRC64;

Query Match 8.2%; Score 79.5; DB 2; Length 153;
Best Local Similarity 32.9%; Pred. No. 24;
Matches 27; Conservative 7; Mismatches 35; Indels 13; Gaps 2;

QY 110 GBEIILPRGLETVVECTEDCIKPKVDSDHCFPLPAMEGATILVTKTNDY----- 164
DB 34 GDVRIVASGRPYRVGLCDCKRKHGAL-----FHSAIFPQTAVTVTGETRDYAGRFF 88
QY 165 ---CKSLPAALSATEIEKSISA 183
DB 89 CPGSGSVFARTADEIEVSLGA 110

RESULT 40
ID_FAK2_HUMAN STANDARD; PRT; 1009 AA.
AC Q14289; Q13475; Q14290; Q16709;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
2) (PAK2) (Prolin-rich tyrosine kinase 2) (Cell adhesion kinase
beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
adhesion focal tyrosine kinase).
DE adhesion focal tyrosine kinase.
GN Names=PTK2B; Synonyms=FAK2, PYK2, RAFTK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95379967; PubMed=7544443;
RA Lev S., Moreno H., Martinez R., Canoll P., Peles E., Musacchio J.M.,
RA Florman G.D., Rudy B., Schlessinger J.;
RT "Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of
ion channel and MAP kinase functions.";
RL Nature 376:737-745(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=96435932; PubMed=8838818;
RA Herzog H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
RT "Molecular cloning and assignment of FAK2, a novel human focal
adhesion kinase, to 8p11.2-p22 by nonisotopic in situ hybridization.";
RL Genomics 32:484-486(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=95403356; PubMed=7673154;
RA Sasaki H., Nagura K., Ichino M., Tobiooka H., Kotani K., Sasaki T.;
RT "Cloning and characterization of cell adhesion kinase beta, a novel
protein-tyrosine kinase of the focal adhesion kinase subfamily.";
RL J. Biol. Chem. 270:21206-21219(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=96070905; PubMed=7499242;
RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
RA Fasztor L.M., White R.A., Groopman J.E., Avraham H.;
RT "Identification and characterization of a novel related adhesion focal
tyrosine kinase (RAFTK) from megakaryocytes and brain.";
RL J. Biol. Chem. 270:27742-27751(1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Monocytes;

RE MEDLINE=98211954; PubMed=9545257;
RA Li X., Hunter D., Morris J., Haskill J.S., Earp H.S.;
RT "A calcium-dependent tyrosine kinase splice variant in human
RT monocytes. Activation by a two-stage process involving adherence and a
RL subsequent intracellular signal.";
RN J. Biol. Chem. 273:9361-9364(1998).
[6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N.,
RA Menzel U., Schilbabel M.B., Wen G., Taudien S., Rosenthal A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Wang J., Haig F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RP INTERACTION WITH DDEF2.
RX PubMed=1002920;
RA Andreev J., Simon J.-P., Sabatini D.D., Kam J., Plozman G.,
RA Randazzo P.A., Schlessinger J.;
RT "Identification of a new Pyk2 target protein with Arf-GAP activity.";
RL Mol. Cell. Biol. 19:2338-2350(1999).
[9]
RP PHOSPHORYLATION SITE TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
RX WITH NEPHROCYSTIN.
RX MEDLINE=21396557; PubMed=11493697; DOI=10.1073/pnas.171269898;
RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
RT phosphorylation of Pyk2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
[10]
RP PHOSPHORYLATION SITES TYR-579 AND TYR-580.
RX PubMed=12522270; DOI=10.1073/pnas.2436191100;
RA Salomon A.R., Ficarro S.B., Brill L.M., Brinker A., Phung Q.T.,
RA Ericson C., Sauer K., Brock A., Horn D.M., Schulz P.G., Peters E.C.;
RT "Profiling of tyrosine phosphorylation pathways in human cells using
RT mass spectrometry.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:443-448(2003).
CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
CC and activation of the map kinase signaling pathway. May represent
CC an important signaling intermediate between neurotrophin activated
CC receptors or neurotransmitters that increase calcium flux and the
CC downstream signals that regulate neuronal activity. Interacts with
CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
CC potassium channel protein Kv1.2. Its activation is highly
CC correlated with the stimulation of c-Jun N-terminal kinase
CC activity.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas), PrpNS1 (By
CC similarity), Nephrocystin, DDEF2 and OPHN1L.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
CC induces the membrane-association of the kinase.

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q14289-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q14289-2; Sequence=VSP_004981;
CC levels in amygdala and hippocampus. Low levels in kidney. Also
CC expressed in spleen and lymphocytes.
CC -1- PM: Phosphorylated on tyrosine residues in response to various
CC stimuli that elevate the intracellular calcium concentration, as
CC well as by PKC activation. Recruitment by Nephrocystin to cell
CC matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,
CC adherence to substrata is required for tyrosine phosphorylation
CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
CC lysophosphatidic acid (LPA) also induce autophosphorylation and
CC increase kinase activity (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
CC subfamily.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U33284; AAC50203.1; -;
CC EMBL; L49207; AAB47217.1; -;
CC EMBL; D45853; BAA08289.1; -;
CC EMBL; U43522; AAC05330.1; -;
CC EMBL; S80542; AAB35701.1; -;
CC EMBL; AF311103; -; NOT_ANNOTATED_CDS.
CC EMBL; BC042599; AAB42599.1; -;
CC PIR; S60248; S60248.
CC HSP; Q05397; 1K04.
CC Genew; HGNC:9612; PTK2B.
CC MIM; 601212; -; Cytoplasm; TAS.
CC GO; GO:0005737; Cytoplasm; TAS.
CC GO; GO:0004715; FERM-membrane spanning protein tyrosine kina. .; TAS.
CC GO; GO:0006915; P:apoptosis; TAS.
CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC GO; GO:0006461; P:protein complex assembly; TAS.
CC GO; GO:0006950; P:response to stress; TAS.
CC GO; GO:0007172; P:signal complex formation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR009065; FERM.
CC InterPro; IPR005189; Focal AT.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC Pfam; PF03623; Focal AT; 1.
CC Pfam; PF00069; Kinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00295; B41; 1.
CC SMART; SM00219; TyrKc; 1.
CC PROSITE; PS00660; FERM 1; FALSE NEG.
CC PROSITE; PS00661; FERM 2; FALSE NEG.
CC PROSITE; PS00557; FERM 3; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC KW Tyrosine-protein kinase.
CC Alternative splicing; ATP-binding; Phosphorylation; Transferase;
FT DOMAIN 39 359 FERM.
FT DOMAIN 425 633 Protein kinase.
FT NP_BIND 431 439 ATP (By similarity).
FT

DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00057; FERM 3; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 1009 AA; 115906 MW; 58BA8A046274E7C2 CRC64;

Query Match 8.28; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.11; Pred. No. 1.7e+02;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3

QY 88 EFKNTSGLLGMANIDLEKSR-----TGDEIILPRGLEVTVECTCEDCIKSKPKV 138
DB 249 KFFNT---LAFGANIDETVRCILQGNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
QY 139 DSDHCFPLPAMEGATIL 156
DB 306 RSIRCLPL---EEQAVL 320

RESULT 42
ID AAH36651 PRELIMINARY; PRT; 1009 AA.
AC AAH36651;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE PRK2B protein tyrosine kinase 2 beta, isoform a.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg H., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Strausberg R.;
RA Submitted (Aug-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC036651; AAH36651.1; -;
KW Kinase.
SQ SEQUENCE 1009 AA; 115906 MW; 58BA8A046274E7C2 CRC64;

Query Match 8.28; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.11; Pred. No. 1.7e+02;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3

```

QY 88 EFKNTGSLGLMANIDLEKSR-----TCDEIILPRGLETVVEECTCDDCIKSKPKV 138
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 KFFNT---LAGFANIQQTYRCLEIQQNWIITVDLVIGPKIRQLTSQDKPTCLAEFKQI 305
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 139 DSDHCFPLPAMEGATIL 156
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 306 RSIRCLPL---EGQAVL 320
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 43
Q26489 PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sf9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to peptidase family S8.
DR EMBL; 268888; CA93116.1; -.
DR PIR; T43251; T43251.
DR HSSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR011031; Multihem cyt.
DR InterPro; IPR000209; Pept S8 S53.
DR InterPro; IPR009020; Prot_inh_propept.
DR InterPro; IPR002884; Ppirtcnconverter.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00082; Peptidase S8; 1.
DR Pfam; PF01483; P proproteain; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 3.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 1299 AA; 142019 MW; 4C3799C7BEC572AB CRC64;

Query Match 8.2%; Score 79.5; DB 2; Length 1299;
Best Local Similarity 24.1%; Pred. No. 2.3e+02;
Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEYFDSLHACIPCOLRCS-----SNTPLTCQRYCNAS-----VTNSVKTNAIL-W 57
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1150 CSRLRIDLRLNNQVCP---CSRGVNTSPPTDC-CHCNPEGECINSSVAGKRRAEW 1205
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 58 TGLGLS-----LIISLAV-----EVLMLFLARKISSEPLKDFKNTGSGLLGMAN 101
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1206 GALHTAFSADAAPSVAVVTVIACAAVGLFITVLVLQAHSPREKTRKTSVFG----- 1259
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 102 IDLEKSTGTDEIILPR-GLEYTVEECTCDDCIKSKPKVSDH 142
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 1260 --VEYSR-----LPRTDVDFTV-----LTSCTDQEGPVEYEH 1289
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 44
Q7R6V0 PRELIMINARY; PRT; 333 AA.
AC Q7R6V0;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative Yir3 protein.
GN Name=PY07843;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC PUBMED=12368865;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC 1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002953; EAA20383.1; -.
DR InterPro; IPR006477; Yir_bir_cir.
DR Pfam; PF06022; Cir_Bir_Yir; 1.
DR TIGRFAMs; TIGR01530; Yir-bir-cir_Pla; 1.
SQ SEQUENCE 333 AA; 39110 MW; A3D4B87FF16D7391 CRC64;

Query Match 8.2%; Score 79; DB 2; Length 333;
Best Local Similarity 27.1%; Pred. No. 60;
Matches 57; Conservative 24; Mismatches 79; Indels 50; Gaps 10;

QY 11 NEYFDSLHACIPQLRCSNTPPLTCQRYCNASVNSVKGYN-----AILWTCGLSL 64
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 35 NKYCDS--NOCHSDYDRISAGCLYLLDQLYKDSGVIPSPKNSPNYIVDYILWLSYMLNL 92
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 65 IISLAVFVLMFLRLKISS-----EPLKDFKNTGS-----GLLGMANIDLEKS-RTGD 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 INSKEDNITDFYGSHINSCKYKTEISELKNHYDIGNYNYKGL-----IDRRKDFLYMD 147
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 112 EILPR-----GLEYTVEEC-----TCEDCIKSKPKVDSHPCHPLPAMEBG 152
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 148 SNIVPKFYAEFKLLCNLYNELDYNKNCKEYKLNKDNSEFPKFKYKELKDSITNSSPYKEML 207
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 153 AILVTYTKNDY---CKSLPAALSATEIK 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 STILL--TDYNDPKKCNLSILSYLSAKEK 235
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 45
Q802S1 PRELIMINARY; PRT; 1200 AA.
AC Q802S1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SMC2 protein.
GN Name=smc2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Percomorphs; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cobbe N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 CC EMBL; AJ534333; CAD58848.2; -;
 DR HSSP; P04268; 11C2.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
 DR GO; GO:0007059; P:chromosome segregation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR003405; SMC_C.
 DR InterPro; IPR010935; SMC_hinge.
 DR InterPro; IPR003395; SMC_N.
 DR Pfam; PF02483; SMC_C; 1.
 DR Pfam; PF06470; SMC_hinge; 1.
 DR Pfam; PF02463; SMC_N; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
 KW ATP-binding.
 SQ SEQUENCE 1200 AA; 135735 MW; 5243949FD948321EF CRC64;
 Query Match 8.2%; Score 79; DB 2; Length 1200;
 Best Local Similarity 32.3%; Pred. No. 2.3e+02;
 Matches 21; Conservative 8; Mismatches 36; Indels 0; Gaps 0;
 QY 77 LRKTSPLDPEKPNQSGLLGMANIDLEKSRGTDEILPRGLVTVETCECDIKSKP 136
 DB 578 LNKISATLDRVNTAKSLVGRANVTALSLVGEADLRKMYVFGSLVCDTLDNK 637
 QY 137 KVDSD 141
 DB 638 KVAFD 642
 RESULT 46
 ID T13X HUMAN STANDARD; PRT; 293 AA.
 AC O14836;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN Name=TNFRSF13B; Synonyms=TACI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; PubMed=93111921;
 RA von Buelow G.-U., Bram R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily.";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.H.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP FUNCTION
 RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
 RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
 RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
 RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
 RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
 RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
 RT high affinity receptor for TNF family members APRIL and BlyS.";
 RL J. Biol. Chem. 275:35478-35485(2000).
 RN [4]
 RP FUNCTION
 RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 RN [5]
 RP INTERACTIONS WITH TRAF2 AND TRAF5.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.Y., Boyle W.J., Hu H.;
 RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143(2000).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity.
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLG with its C-terminus.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
 CC intestine and peripheral blood leukocytes. Expressed in resting B-
 CC cells and activated T-cells, but not in resting T-cells.
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF023614; AAC51790.1; -;
 CC EMBL; BC028072; AAH28072.1; -;
 DR HSSP; O9Y275; 100D.
 DR Genew; HGNC:18153; TNFRSF13B.
 DR MIM; 604507; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPRO01368; TNFR c6
DR PROSITE; PS00452; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.
KW DOMAIN 1 165 Extracellular (Potential).
FT TRANSMEM 166 186 Signal-anchor for type III membrane protein (Potential).
FT DOMAIN 187 293 Cytoplasmic (Potential).
FT REPEAT 33 67 TNFR-Cys 1.
FT REPEAT 70 104 By similarity.
FT DISULFID 34 47 By similarity.
FT DISULFID 50 62 By similarity.
FT DISULFID 54 66 By similarity.
FT DISULFID 71 86 By similarity.
FT DISULFID 89 100 By similarity.
FT DISULFID 93 104 By similarity.
FT CARBOHYD 128 128 N-linked (GlcNAc...) (Potential).
FT CONFLICT 251 251 P -> L (in Ref. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17ASEB CRC64;

Query Match 8.1%; Score 78.5; DB 1; Length 293;
Best Local Similarity 19.9%; Pred. No. 59;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEVDSLHACIPCOLRCSSTNPPLTCORYCNASVTSVKT--NAILWTCLGLSLI 65
DB 34 CPSEQYDPLGLTGMCSKTTICNHOS-QRTCAAFCSRSLSCRKEQKGYDHLRLDCISCAI 92

QY 66 I-----SLAVFLMFL-----LRKISSEPLKDFKNTGSLGWMANIDLEKS---- 107
DB 93 CGQHPKQCAFCENKLRSPVNLPELRQRSGEVNNSDNGR-YQGLEHKGSGASPALP 151

QY 108 ---RTGDEIILPRG-----LEVTVECTEDCIKSKP-----KVD 139
DB 152 GLKLSADQVALVYSTGLICLCAVLVACFLKRGDPCSCQP--RSRPRQSPAKSS 209

QY 140 SDHCFPLPAMEEGATILVTTKNDYC 165
DB 210 QDH-----AMEAGSVSTSPFVETC 230

RESULT 47
Q8VFW0 PRELIMINARY; PRT; 314 AA.
ID Q8VFW0
AC Q8VFW0
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Olfactory receptor MOR202-16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21864068; PubMed=11875048;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L., Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory receptor gene families."
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.;

Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY073405; AAL61068.1; .
GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPRO00276; GPCR Rhodopsin.
DR InterPro; IPRO00725; Olfact_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 34987 MW; DE5CDDF63E3B2FD8 CRC64;

Query Match 8.1%; Score 78.5; DB 2; Length 314;
Best Local Similarity 30.4%; Pred. No. 63;
Matches 31; Conservative 15; Mismatches 41; Indels 15; Gaps 6;

QY 8 CSQNEVDSLHACIPCOLRCSSTNPPLTCORYCNASVTSVKT--NAILWTCLGLSLI 59
DB 146 CYMGILQSSIRHVALAFCLSFNCNVINHFCDIPPL-LDISCSDTYTNEI--TVILIGT 202

QY 59 CLG-LSLIISLAVFLMFL--LRKISSEPLKDFKNTGSLGL 97
DB 203 CDGILTLVILNTYLLIFAILMRVSEARAFSTCASHLI 244

RESULT 48
MJK2_METJ2 STANDARD; PRT; 343 AA.
ID MJK2_METJ2
AC Q58752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable potassium channel protein 2 (MjK2).
GN OrderedLocusNames=MJ1357;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."
RL Science 273:1058-1073(1996).
RN [2]
RP FUNCTION.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=22744766; PubMed=12860407;
RA Hellmer J., Zeilinger C.;
RT "MjK1, a K+ channel from M. jannaschii, mediates K+ uptake and K+ sensitivity in E. coli."
RL FEBS Lett. 547:165-169(2003).
CC -!- FUNCTION: Probable potassium channel protein.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Contains 1 trkA/RCK domain.
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CC -----
CC EMBL; U67575; AAB93365.1; -.
CC PIR; D64469; D64469.
CC HSSP; O27564; ILNQ.
CC TIGR; MJ1357; -.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR006037; TrkA_C.
DR InterPro; IPR003148; TrkA_N.
DR Pfam; PF02080; TrkA_C; 1.
DR Pfam; PF02254; TrkA_N; 1.
KW Complete proteome; Ion transport; Ionic channel; Potassium;
KW Potassium channel; Potassium transport; Transmembrane; Transport.
FT DOMAIN 1 7 Potassium Cytoplasmic (Potential).
FT TRANSMEM 8 28 Potential.
FT DOMAIN 29 61 Extracellular (Potential).
FT TRANSMEM 62 82 Potential.
FT DOMAIN 83 343 Cytoplasmic (Potential).
FT SITE 46 51 Selectivity filter (By similarity).
SQ SEQUENCE 343 AA; 38883 MW; 61231B0C001B54C4 CRC64;
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Best Local Similarity 20.4%; Pred. No. 69;
Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;
QY 12 EYDLSLHACIPQCRSSNTPPLTCQRYCNASVTSVKGNTNAILTCGLSLIISLAVF 71
DB 32 DYFALYSVI-----TITTYGYDPTPKFLGRTLTVVLCVGVGIVWLFSL 80
QY 72 VLMFL-----LRKISS--EPLKDEPKNTGSGLLGMA-----NIDLEKSRGTG 111
DB 81 IAEFIVEGKEPFEVRLKMKMKIKLKHVYICGYGLGKVGKGFTEENIPFIADINE 140
QY 112 EII-----LPRGLETVVECTCEDCKSKPKV-----PSDHCF-PLPAMEEG 152
DB 141 DVLKEERYKPYDKPLXIVGDAKKEVLK-RAKIDKAKGLIATLPDADNVFLTARELN 199
QY 153 ATILVTTKND 163
DB 200 PNILITAKADE 210
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RESULT 49
Q9H677 PRELIMINARY; PRT; 485 AA.
AC Q9H677;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ22531.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Ooyashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isoigai T., Sugano S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026184; BAB15387.1; -.
DR InterPro; IPR007110; Ig-like.
SQ SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
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Best Local Similarity 26.3%; Pred. No. 99;
Matches 35; Conservative 17; Mismatches 48; Indels 33; Gaps 6;
QY 47 NSVKGNTNAILWTCLGLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGS-----GLLGM 99
DB 185 NRISSVSIFLYGLPLGLPLLS-----TWEQPMWTFPKDTSLSLWKKYHLCMI 232
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QY 100 ANIDLEKSRGTGEIILPRGLETVVECTCEDCKSKPK-----VSDHCFPLPAME 150
DB 233 PNLDLNLDR---DLVLP-DVSYQVSESEEDSQOTMDPQQTLLFLFVDFHSAFPVQOME 288
QY 151 -EGATILVTTKTN 162
DB 289 INGVYTLTTHLN 301
RESULT 50
Q8N670 PRELIMINARY; PRT; 522 AA.
AC Q8N670;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ22531.
GN Names=FLJ22531;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mundy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028240; AAH28240.1; -.
DR InterPro; IPR007110; Ig-like.
KW Hypothetical protein.
SQ SEQUENCE 522 AA; 58061 MW; C7A9100E2E10E9E1 CRC64;
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Best Local Similarity 26.3%; Pred. No. 11e+02;
Matches 35; Conservative 17; Mismatches 48; Indels 33; Gaps 6;
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DB 185 NRISSVSIFLYGLPLGLPLLS-----TWEQPMWTFPKDTSLSLWKKYHLCMI 232
QY 100 ANIDLEKSRGTGEIILPRGLETVVECTCEDCKSKPK-----VSDHCFPLPAME 150
DB 233 PNLDLNLDR---DLVLP-DVSYQVSESEEDSQOTMDPQQTLLFLFVDFHSAFPVQOME 288
QY 151 -EGATILVTTKTN 162
DB 289 INGVYTLTTHLN 301
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Search completed: January 28, 2005, 19:57:02
Job time : 220.385 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:52:54 ; Search time 163.743 Seconds
(without alignments)
405.985 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964

Sequence: 1 MLQWAGCQNEYPDSLHA.....CKSLPALSATEIKSISAR 184

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 964 | 100.0 | 184 | 13 | US-10-077-438-1 |
| 2 | 964 | 100.0 | 184 | 13 | US-10-077-438-7 |
| 3 | 964 | 100.0 | 184 | 13 | US-10-077-137-1 |
| 4 | 964 | 100.0 | 184 | 13 | US-10-077-137-7 |
| 5 | 964 | 100.0 | 184 | 14 | US-10-068-725-2 |
| 6 | 964 | 100.0 | 184 | 14 | US-10-151-882-47 |
| 7 | 964 | 100.0 | 184 | 14 | US-10-115-192-8 |
| 8 | 964 | 100.0 | 184 | 14 | US-10-008-063-7 |
| 9 | 964 | 100.0 | 184 | 14 | US-10-152-363A-27 |
| 10 | 964 | 100.0 | 184 | 14 | US-10-216-074-11 |
| 11 | 964 | 100.0 | 184 | 14 | US-10-087-080-39 |
| 12 | 964 | 100.0 | 184 | 17 | US-10-742-634-9 |
| 13 | 950 | 98.5 | 181 | 9 | US-09-854-864-5 |

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| 14 | 950 | 98.5 | 181 | 9 | US-09-855-158-5 | Sequence 5, Appli |
| 15 | 572 | 59.3 | 185 | 9 | US-09-854-864-11 | Sequence 11, Appl |
| 16 | 572 | 59.3 | 185 | 9 | US-09-855-158-11 | Sequence 11, Appl |
| 17 | 572 | 59.3 | 185 | 14 | US-10-216-074-17 | Sequence 17, Appl |
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| 19 | 323 | 33.5 | 58 | 9 | US-09-855-158-21 | Sequence 21, Appl |
| 20 | 311.5 | 32.3 | 117 | 9 | US-09-854-864-12 | Sequence 12, Appl |
| 21 | 311.5 | 32.3 | 117 | 9 | US-09-855-158-12 | Sequence 12, Appl |
| 22 | 286.5 | 29.7 | 302 | 14 | US-10-115-192-12 | Sequence 12, Appl |
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| 24 | 286 | 29.7 | 283 | 9 | US-09-855-158-9 | Sequence 9, Appli |
| 25 | 284 | 29.5 | 51 | 9 | US-09-854-864-6 | Sequence 6, Appli |
| 26 | 284 | 29.5 | 51 | 9 | US-09-855-158-6 | Sequence 6, Appli |
| 27 | 264 | 27.4 | 207 | 13 | US-10-077-438-3 | Sequence 3, Appli |
| 28 | 264 | 27.4 | 207 | 13 | US-10-077-137-3 | Sequence 3, Appli |
| 29 | 201 | 20.9 | 34 | 9 | US-09-854-864-7 | Sequence 7, Appli |
| 30 | 201 | 20.9 | 34 | 9 | US-09-855-158-7 | Sequence 7, Appli |
| 31 | 201 | 20.9 | 81 | 9 | US-09-854-864-13 | Sequence 13, Appl |
| 32 | 201 | 20.9 | 81 | 9 | US-09-855-158-13 | Sequence 13, Appl |
| 33 | 187 | 19.4 | 281 | 9 | US-09-854-864-10 | Sequence 10, Appl |
| 34 | 187 | 19.4 | 281 | 9 | US-09-855-158-10 | Sequence 10, Appl |
| 35 | 158 | 16.4 | 42 | 14 | US-10-145-206-197 | Sequence 197, App |
| 36 | 116.5 | 12.1 | 175 | 14 | US-10-008-063-13 | Sequence 13, Appl |
| 37 | 116.5 | 12.1 | 175 | 15 | US-10-380-703-9 | Sequence 9, Appli |
| 38 | 116.5 | 12.1 | 175 | 16 | US-10-469-420-1 | Sequence 1, Appli |
| 39 | 104 | 10.8 | 21 | 9 | US-09-854-864-8 | Sequence 8, Appli |
| 40 | 104 | 10.8 | 21 | 9 | US-09-855-158-8 | Sequence 8, Appli |
| 41 | 100 | 10.4 | 185 | 14 | US-10-251-947-2 | Sequence 2, Appli |
| 42 | 94.5 | 9.8 | 185 | 15 | US-10-380-703-5 | Sequence 5, Appli |
| 43 | 93 | 9.6 | 184 | 13 | US-10-087-192-984 | Sequence 984, App |
| 44 | 93 | 9.6 | 184 | 14 | US-10-008-063-2 | Sequence 2, Appli |
| 45 | 93 | 9.6 | 184 | 14 | US-10-152-363A-60 | Sequence 60, Appl |
| 46 | 93 | 9.6 | 184 | 15 | US-10-380-703-10 | Sequence 10, Appl |
| 47 | 93 | 9.6 | 184 | 17 | US-10-742-634-5 | Sequence 5, Appli |
| 48 | 93 | 9.6 | 266 | 15 | US-10-380-703-7 | Sequence 7, Appli |
| 49 | 91 | 9.4 | 171 | 14 | US-10-251-947-4 | Sequence 4, Appli |
| 50 | 91 | 9.4 | 171 | 14 | US-10-251-947-7 | Sequence 7, Appli |
| 51 | 90.5 | 9.4 | 170 | 14 | US-10-251-947-6 | Sequence 6, Appli |
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| 53 | 86.5 | 9.0 | 858 | 14 | US-10-099-323-135 | Sequence 135, App |
| 54 | 86.5 | 9.0 | 858 | 15 | US-10-044-564-135 | Sequence 135, App |
| 55 | 86.5 | 9.0 | 867 | 10 | US-09-970-944-37 | Sequence 37, Appl |
| 56 | 86.5 | 9.0 | 867 | 14 | US-10-099-323-134 | Sequence 134, App |
| 57 | 86.5 | 9.0 | 867 | 15 | US-10-044-564-134 | Sequence 134, App |
| 58 | 84 | 8.7 | 332 | 14 | US-10-152-363A-62 | Sequence 62, Appl |
| 59 | 83.5 | 8.7 | 404 | 15 | US-10-258-368-15 | Sequence 15, Appl |
| 60 | 83 | 8.6 | 348 | 14 | US-10-152-363A-54 | Sequence 54, Appl |
| 61 | 81.5 | 8.5 | 186 | 14 | US-10-251-947-14 | Sequence 14, Appl |
| 62 | 80.5 | 8.4 | 441 | 15 | US-10-365-620-39 | Sequence 39, Appl |
| 63 | 79.5 | 8.2 | 293 | 9 | US-09-779-050A-42 | Sequence 42, Appl |
| 64 | 79.5 | 8.2 | 1009 | 8 | US-08-987-689A-2 | Sequence 2, Appli |
| 65 | 79.5 | 8.2 | 1009 | 14 | US-10-292-524-2 | Sequence 2, Appli |
| 66 | 79.5 | 8.2 | 1009 | 14 | US-10-325-430-9 | Sequence 9, Appli |
| 67 | 79.5 | 8.2 | 1009 | 15 | US-10-464-805-1 | Sequence 1, Appli |
| 68 | 79.5 | 8.2 | 1009 | 16 | US-10-620-052A-8 | Sequence 8, Appli |
| 69 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1562 | Sequence 1562, Ap |
| 70 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1563 | Sequence 1563, Ap |
| 71 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1564 | Sequence 1564, Ap |
| 72 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1565 | Sequence 1565, Ap |
| 73 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1566 | Sequence 1566, Ap |
| 74 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1567 | Sequence 1567, Ap |
| 75 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1568 | Sequence 1568, Ap |
| 76 | 79.5 | 8.2 | 1009 | 17 | US-10-473-127-1569 | Sequence 1569, Ap |
| 77 | 78.5 | 8.1 | 293 | 9 | US-09-879-919-22 | Sequence 22, Appl |
| 78 | 78.5 | 8.1 | 293 | 9 | US-09-854-864-14 | Sequence 14, Appl |
| 79 | 78.5 | 8.1 | 293 | 9 | US-09-855-158-14 | Sequence 14, Appl |
| 80 | 78.5 | 8.1 | 293 | 9 | US-09-961-376-2 | Sequence 2, Appli |
| 81 | 78.5 | 8.1 | 293 | 10 | US-09-302-863-2 | Sequence 2, Appli |
| 82 | 78.5 | 8.1 | 293 | 13 | US-09-855-564-2 | Sequence 2, Appli |
| 83 | 78.5 | 8.1 | 293 | 13 | US-10-087-192-1650 | Sequence 1650, Ap |
| 84 | 78.5 | 8.1 | 293 | 13 | US-10-084-971-2 | Sequence 2, Appli |
| 85 | 78.5 | 8.1 | 293 | 14 | US-10-068-723-4 | Sequence 4, Appli |
| 86 | 78.5 | 8.1 | 293 | 14 | US-10-151-882-46 | Sequence 46, Appl |

Sequence 2, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 27, Appli
Sequence 12, Appli
Sequence 2773, Ap
Sequence 166150,
Sequence 141214,
Sequence 43, Appli
Sequence 8, Appli

87 78.5 8.1 293 14 US-10-293-816-2
88 78.5 8.1 293 14 US-10-008-063-8
89 78.5 8.1 293 14 US-10-152-363A-2
90 78.5 8.1 293 14 US-10-268-951-22
91 78.5 8.1 293 15 US-10-258-368-1
92 78.5 8.1 293 15 US-10-618-797-4
93 78.5 8.1 293 17 US-10-742-634-7
94 78.5 8.1 293 17 US-10-748-112-27
95 78.5 8.1 301 15 US-10-258-368-12
96 78.5 8.1 301 15 US-10-264-237-2773
97 78.5 8.1 606 16 US-10-437-963-166150
98 78.5 8.1 2984 16 US-10-437-963-141214
99 78.5 8.1 1091 9 US-09-779-050A-43
100 77.5 8.0 334 15 US-10-258-368-8

ALIGNMENTS

RESULT 1
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoop, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

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Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60

Qy 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 2

US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoop, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match 100.0%; Score 964; DB 13; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60
Db 1 MLQAGQCSQNEYFDSLHACIPQLRCSNTPPLTCQRYCNASVTNSVKGTTNAILWTCL 60

Qy 61 GLSLIISLAVFLMFLRLKISSEPLKDFKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
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Qy 121 YTVBECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 3
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoop, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684

US-10-151-882-47

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 7

US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens

US-10-115-192-8

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 8

US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1

GENERAL INFORMATION:

; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Heme, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-008-063-7

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCORYCNASVTNSVKGTHAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
Db 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Qy 181 ISAR 184
Db 181 ISAR 184

RESULT 9

US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-152-363A-27

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GLSLIISLAVFVLMFLRLKISSEPLKDEPKNTGSGLLGMANIDLEKSRGTGDEIILPRGLE 120
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Qy 121 YTVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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Qy 181 ISAR 184
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181 ISAR 184

Db 181 ISAR 184

RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US2003014845A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120
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61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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Qy 181 ISAR 184
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181 ISAR 184

Db 181 ISAR 184

RESULT 11
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1el Methods of Diagnosis of Metastatic Colorectal
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-0008400S
; CURRENT APPLICATION NUMBER: US/10/087,080
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555

; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39

Query Match 100.0%; Score 964; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLPTCQRYCNASVTNSVKGTTNAILWTCL 60
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|
61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

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Qy 181 ISAR 184
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181 ISAR 184

Db 181 ISAR 184

RESULT 12
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match 100.0%; Score 964; DB 17; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLPTCQRYCNASVTNSVKGTTNAILWTCL 60
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1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLPTCQRYCNASVTNSVKGTTNAILWTCL 60

Qy 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120
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61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120

Db 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120
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|
61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSLGLGMANIDLEKSRGTDEIILPRGLE 120

Qy 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180

Db 121 YTVBECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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Db 181 ISAR 184

RESULT 13
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 98.5%; Score 950; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 7.1e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORYCNASVTNSVKGTTNAILWTCIGLS 63
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORYCNASVTNSVKGTTNAILWTCIGLS 60
QY 64 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 123
Db 61 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 120
QY 124 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
QY 184 R 184
Db 181 R 181

RESULT 14
US-09-855-158-5
; Sequence 5, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-855-158-5
Query Match 98.5%; Score 950; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 7.1e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORYCNASVTNSVKGTTNAILWTCIGLS 63
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORYCNASVTNSVKGTTNAILWTCIGLS 60
QY 64 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 123
Db 61 LIISLAVFVLMFLRLKISSEPLKDEFKNTGSLGGMANIDLEKSRGTDEIILPRGLETV 120
QY 124 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
Db 121 EECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
QY 184 R 184
Db 181 R 181

RESULT 15
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 59.3%; Score 572; DB 9; Length 185;
Best Local Similarity 62.6%; Pred. No. 3.4e-50;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCORYCNASVTNSVKGTTNAILWTCIGLS 63
Db 1 MAQCQCFHSEYFDSLHACKPCHLRCN--PPATCQPCYCDPSVTSSVKGTYTVLWIFLGLT 58
QY 64 LIISLAVFVLMFLRLKISSEPLKDEFKN---TGSGLGGMANIDLEKSRGTDEIILPRGL 119
Db 59 LVLSLALFTISFLRLKQNFPEALKDEPQSGQLDGSQALDKADTELTRIRAGDDRIIPRSL 118
QY 120 EYTVBECTCEDCIKSPKVDSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db 119 EYTVBECTCEDCVKSPKGDSDHFFPLPAMEGATILVTTKTGDYCKSSVPTALQSVMG 178
QY 178 EKSISAR 184
Db 179 EKPHTHR 185
RESULT 16
US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1

| | | | |
|--|-----|---|-----|
| QY | 64 | LIISLAVFVLMFLRLKISSEPLKDFKN-----TGSGLLGMANIDLEKSRGTGDSIILPRGL | 119 |
| DB | 59 | LVLISLALFTISFLLRKONPEALKDEPQSPQLDGSQALDKADTELTRIRAGDDRIIPRSL | 118 |
| QY | 120 | EYTVESCTCEDCKSKPKVDHCFPLPAMEEGATILVTTKTDYCK-SLPAAL-SATEI | 177 |
| DB | 119 | EYTVESCTCEDCVKSKPKGSDHFFPLPAMEEGATILVTTKTGDYKGSVPTALQSVGMG | 178 |
| QY | 178 | EKSISAR | 184 |
| DB | 179 | EXPHTR | 185 |
| RESULT 18 | | | |
| US-09-854-864-21 | | | |
| ; Sequence 21, Application US/09854864 | | | |
| ; Patent No. US20020081296A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: THEILL, LARS EYDE | | | |
| ; APPLICANT: YU, GANG | | | |
| ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, | | | |
| ; TITLE OF INVENTION: BLYS/AGP-3, AND TACI | | | |
| ; FILE REFERENCE: A-686B | | | |
| ; CURRENT APPLICATION NUMBER: US/09/854,864 | | | |
| ; CURRENT FILING DATE: 2001-09-11 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/204,039 | | | |
| ; PRIOR FILING DATE: 2000-05-12 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/214,591 | | | |
| ; PRIOR FILING DATE: 2000-06-27 | | | |
| ; NUMBER OF SEQ ID NOS: 31 | | | |
| ; SOFTWARE: Patentin version 3.1 | | | |
| ; SEQ ID NO 21 | | | |
| ; LENGTH: 58 | | | |
| ; TYPE: PRT | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-09-854-864-21 | | | |
| Query Match 33.5%; Score 323; DB 9; Length 58; | | | |
| Best Local Similarity 100.0%; Pred.No. 2.3e-25; | | | |
| Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 8 | CSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTTNAILWTCIGLSLI | 65 |
| DB | 1 | CSQNEYFDSLLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTTNAILWTCIGLSLI | 58 |
| RESULT 19 | | | |
| US-09-855-158-21 | | | |
| ; Sequence 21, Application US/09855158 | | | |
| ; Publication No. US20020086018A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: THEILL, LARS EYDE | | | |
| ; APPLICANT: YU, GANG | | | |
| ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, | | | |
| ; TITLE OF INVENTION: 3, AND TACI | | | |
| ; FILE REFERENCE: A-686A | | | |
| ; CURRENT APPLICATION NUMBER: US/09/855,158 | | | |
| ; CURRENT FILING DATE: 2001-09-11 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/214,591 | | | |
| ; PRIOR FILING DATE: 2000-06-27 | | | |
| ; PRIOR APPLICATION NUMBER: US 60/204,039 | | | |
| ; PRIOR FILING DATE: 2000-05-12 | | | |
| ; NUMBER OF SEQ ID NOS: 30 | | | |
| ; SOFTWARE: Patentin version 3.1 | | | |
| ; SEQ ID NO 21 | | | |
| ; LENGTH: 58 | | | |
| ; TYPE: PRT | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-09-855-158-21 | | | |
| Query Match 33.5%; Score 323; DB 9; Length 58; | | | |
| Best Local Similarity 100.0%; Pred.No. 2.3e-25; | | | |

```

Best Local Similarity 61.5%; Pred. No. 8.4e-24;
Matches 96; Conservative 4; Mismatches 7; Indels 49; Gaps 19;

QY 9 SONEYFDSLHACIPCOLRCSNSTPPLTCORYCNASVTNSVKGTTNAILWTCLGLSLIISL 68
Db 2 AQCEYFDSLHAC-PC-LRCS-----PPTCQ-YC--SVT-SVKGT---LW--LGL---LSL 43
QY 69 AVFVLMFLLRKISSSEPLKDFKNTGSGLLGGMANIDLEKSRGTGDEIILPRGLETVBECTC 128
Db 44 A-----FLLARK---ELKDE-----GSLAL-----RGD---IPR-LETVBECTC 76
QY 129 EDCIKKPKVDSHCHPPLPAMEGATILVTTKNDY 164
Db 77 EDC-KSKPK-DSDH-FPLPAMEGATILVTTKT-DY 108

RESULT 22
US-10-115-192-12
; Sequence 12, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: Animal Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-12

Query Match 29.7%; Score 286.5; DB 14; Length 302;
Best Local Similarity 39.9%; Pred. No. 1e-20;
Matches 81; Conservative 13; Mismatches 54; Indels 55; Gaps 8;

QY 1 MLOAGQCSQNEYFDSLHACIPCOLRCSNSTPPLTCORYCNASVTNSVKGTTNAILWTCL 60
Db 24 MLOAGQCSQNEYFDSLHACIPCOLRCSNSTPPLTCORYCNASVTNSVKGVDK-THTC- 81
QY 61 GLSLIISLAVFVLMFLLRKISSSEPLKDFKNTGSGLLGGMANIDLEKSRGTGDEIILPRGLE 120
Db 82 -----PPC-----PAPELLGGPSVFLPFPKFDILMISRTPE 113
QY 121 YTVBECTCDDCIKSPKVDSD-----HCFPLPAMEE-----GATILVTTKTNDY-- 164
Db 114 VT---CVVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNL 170
QY 165 -----CKSLPALSALETEKHSIS 182
Db 171 GKEYKCKVSNKALPA-PIEKTIS 192

RESULT 23
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864

```

; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match 29.7%; Score 286; DB 9; Length 283;

Best Local Similarity 37.6%; Pred. No. 1e-20;
Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;

Qy 4 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTAAILWTCGLS 63

Db 1 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTA----- 51

Qy 64 LIISLAVFLMFLLRKISSEPLKDFKNTGSG-----LLGMANIDLEKSRGTG 110

Db 52 -----GGGGDKTHTCPPCAPPELLGGPSVFLFPKPK 84

Qy 111 DEILPRGLEVTVECTCEDCIKPKVDS-----HCFPLPAMEE-----GATIL 156

Db 85 DTLMSRTPVET---CVVVDVSHEDPVEKFNWYVDGVEVHNNAKTKPREEQNSTYRVVSV 141

Qy 157 VTTKTNDY-----CKSLPAALSATEIEKSI 182

Db 142 LTVLHQDLWNGKEYCKVSNKALPA-PIEKTIS 173

RESULT 24

US-09-855-158-9

; Sequence 9, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 283

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-9

Query Match

Best Local Similarity 37.6%; Pred. No. 1e-20;

Matches 80; Conservative 12; Mismatches 47; Indels 74; Gaps 7;

Qy 4 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTAAILWTCGLS 63

Db 1 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTA----- 51

Qy 64 LIISLAVFLMFLLRKISSEPLKDFKNTGSG-----LLGMANIDLEKSRGTG 110

Db 52 -----GGGGDKTHTCPPCAPPELLGGPSVFLFPKPK 84

Qy 111 DEILPRGLEVTVECTCEDCIKPKVDS-----HCFPLPAMEE-----GATIL 156

Db 85 DTLMSRTPVET---CVVVDVSHEDPVEKFNWYVDGVEVHNNAKTKPREEQNSTYRVVSV 141

Qy 157 VTTKTNDY-----CKSLPAALSATEIEKSI 182

Db 142 LTVLHQDLWNGKEYCKVSNKALPA-PIEKTIS 173

RESULT 25

US-09-854-864-6

; Sequence 6, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-6

Query Match

Best Local Similarity 100.0%; Pred. No. 1.9e-21;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTA 54

Db 1 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTA 51

RESULT 26

US-09-855-158-6

; Sequence 6, Application US/09855158

; Publication No. US20020086018A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL

; FILE REFERENCE: A-686A

; CURRENT APPLICATION NUMBER: US/09/855,158

; CURRENT FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-855-158-6

Query Match

Best Local Similarity 100.0%; Pred. No. 1.9e-21;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTA 54

Db 1 MAGQCSONEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKGTA 51

RESULT 27

```
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR FILING DATE: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match      27.4%; Score 264; DB 13; Length 207;
Best Local Similarity 63.9%; Pred. No. 1.2e-18;
Matches 53; Conservative 2; Mismatches 0; Indels 28; Gaps 2;

Qy 1 MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPTLCLHACIPQCLRCSSNTPTLTCQRY 40
Db 39 MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPTLCLHACIPQCLRCSSNTPTLTCQRY 98

Qy 41 CNASVTNSVKG-----TNAI 55
Db 99 CNASVTNSVKGQRYCNASVTNSV 121

RESULT 28
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7
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```
; ORGANISM: homo sapien
US-10-077-137-3

Query Match      27.4%; Score 264; DB 13; Length 207;
Best Local Similarity 63.9%; Pred. No. 1.2e-18;
Matches 53; Conservative 2; Mismatches 0; Indels 28; Gaps 2;

Qy 1 MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPTLCLHACIPQCLRCSSNTPTLTCQRY 40
Db 39 MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPTLCLHACIPQCLRCSSNTPTLTCQRY 98

Qy 41 CNASVTNSVKG-----TNAI 55
Db 99 CNASVTNSVKGQRYCNASVTNSV 121

RESULT 29
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      20.9%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTCQRYC 34

RESULT 30
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7
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```
Query Match      20.9%; Score 201; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e-13;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 31
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      20.9%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 32
US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-855-158-13

Query Match      20.9%; Score 201; DB 9; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
```

```
RESULT 33
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match      19.4%; Score 187; DB 9; Length 281;
Best Local Similarity 29.8%; Pred. No. 1.4e-10;
Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;

Qy 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNA5VTNSVKGTNAILWTCLGLS 63
Db 1 MAQCCFHSEYFDSLHACKCHLRCSN--PPTCQPYCDPSVTSSVKGK----- 47
Qy 64 LIISLAVFLMFLRLKISSEPLKDFKNTGSG-----YLGWANIIDLKSR 108
Db 48 -----YTGSGGDKTHCTCPAPPELLGSPVFLFPK 80
Qy 109 TGDEIILPRGLVTVBECTCEDCIKSPKVDSD-----HCFPLPAMBE-----GAT 154
Db 81 PKDTLMISRTPEVT---CVVDVSHEDPEVKFNWYDGVGVHNAKTRPREQYNSTVRVV 137
Qy 155 ILVTTKINDY-----CKSLPAALSATEIEKIS 182
Db 138 SVLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTI 171

RESULT 34
US-09-855-158-10
; Sequence 10, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match      19.4%; Score 187; DB 9; Length 281;
Best Local Similarity 29.8%; Pred. No. 1.4e-10;
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Matches 64; Conservative 17; Mismatches 54; Indels 80; Gaps 8;
Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSNTPLTCORYCNASVTNSVK---GTNAIL 56
Db 1 MAQCFFHSEYFDSLHACKPCHLRCSN--PRATCQPCDPSVTSSVKG-----47
Qy 64 LIISLAVFLVLMFLLRKISSEPLKDFKNTGSG-----LLGGMANIDLEKSR 108
Db 48 -----YTGCGGDKTHTCPPCAPPELLGGPSVFLPPK 80
Qy 109 TGDEILPRGLETVBECTCEDCIKSKPKVDS-----HCFPLPAMEE-----GAT 154
Db 81 PKDTLMISRTPEVT---CVWVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSYRVV 137
Qy 155 ILVTKTNDY-----CKSLPAALSATEIEKIS 182
Db 138 SVLTVLVHODWLNKGEYCKCKVSNKALPA-PIEKTIIS 171

RESULT 35

US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match 16.4%; Score 158; DB 14; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCSQNEYFDSLHACIPCOLRC 28

Db 15 MLQWAGCSQNEYFDSLHACIPCOLRC 42

RESULT 36

US-10-008-063-13
; Sequence 13, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Mouse
US-10-008-063-13

Query Match 12.1%; Score 116.5; DB 14; Length 175;

Best Local Similarity 29.4%; Pred. No. 0.0012;

Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
Qy 7 QCSQNEYFDSLHACIPCOL-----RCSNTPPLTCORYCNASVTNSVK---GTNAIL 56
Db 21 QCNQTECFDPLVRNCVSCSELFHTPDGTGHTSSLEPGTALQPOEGSALRPDVALLVGAPALL 80
Qy 57 WTCIGLSLI--ISLAVFLVLMFLLRKIS--SEPLKDFKNTGSGLLGMANIDLEKSR 111
Db 81 GLILALTLVGLVLSVSRWQQLRTASPTDSEGVOQE-----SLENVFPVSSET--129
Qy 112 EILPRGLETVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKT 161
Db 130 ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSELVTTKT 170

RESULT 37

US-10-380-703-9
; Sequence 9, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S.
; APPLICANT: Ambrose, Christine M.
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-380-703-9

Query Match 12.1%; Score 116.5; DB 15; Length 175;

Best Local Similarity 29.4%; Pred. No. 0.0012;

Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;

Qy 7 QCSQNEYFDSLHACIPCOL-----RCSNTPPLTCORYCNASVTNSVK---GTNAIL 56

Db 21 QCNQTECFDPLVRNCVSCSELFHTPDGTGHTSSLEPGTALQPOEGSALRPDVALLVGAPALL 80

Qy 57 WTCIGLSLI--ISLAVFLVLMFLLRKIS--SEPLKDFKNTGSGLLGMANIDLEKSR 111

Db 81 GLILALTLVGLVLSVSRWQQLRTASPTDSEGVOQE-----SLENVFPVSSET--129

Qy 112 EILPRGLETVBECTCEDCIKSKPKVDSHCFPLPAMEEGATILVTTKT 161

Db 130 ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSELVTTKT 170

RESULT 38

US-10-469-420-1
; Sequence 1, Application US/10469420
; Publication No. US20040170997A1
; GENERAL INFORMATION:
; APPLICANT: IRIE, Shinji, et al.
; TITLE OF INVENTION: TRAF3-BINDING B-CELL-SPECIFIC RECEPTOR
; FILE REFERENCE: 2870-0262P
; CURRENT APPLICATION NUMBER: US/10/469,420
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in v2.1
; SEQ ID NO 1

; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-703-5

Query Match 9.8%; Score 94.5; DB 15; Length 185;
Best Local Similarity 25.8%; Pred. No. 0.24; Indels 49; Gaps 8;
Matches 47; Conservative 22; Mismatches 64; Indels 49; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTPPLTC---QRYCNASVTNSVKGTHAI 55
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78
QY 56 LW---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEK 106
DB 79 LFGAPALLGLALVLALVGLVSWRRQRRLRGASSAEPDGDKDAPEPL----- 128
QY 107 SRTGDEIILPRGLEYTVVECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTT 159
DB 129 ----DKVII---LSPGISDATAPAWPPGDPGTTTP-----GHSVPVPATELGSTELVTT 177
QY 160 KT 161
DB 178 KT 179

RESULT 43
US-10-087-192-984
; Sequence 984, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 984
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-984

Query Match 9.6%; Score 93; DB 13; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTP--PLTCORYCNASVTNSVKGTHAI 56
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78
QY 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
DB 79 FGAPALLGLALVLALVGLVSWRRQRRLRGASSAEPDGDKDAPEPL----- 127
QY 108 RTGDEIILPRGLEYTVVECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTTK 160
DB 128 ---DKVII---LSPGISDATAPAWPPGDPGTTTP-----GHSVPVPATELGSTELVTTK 177
QY 161 T 161
DB 178 T 178

RESULT 44
US-10-008-063-2
; Sequence 2, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Heme, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-2

Query Match 9.6%; Score 93; DB 14; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTP--PLTCORYCNASVTNSVKGTHAI 56
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78
QY 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
DB 79 FGAPALLGLALVLALVGLVSWRRQRRLRGASSAEPDGDKDAPEPL----- 127
QY 108 RTGDEIILPRGLEYTVVECTC-----EDCIKSKPKVDSHCFPLPAMEEGATILVTTK 160
DB 128 ---DKVII---LSPGISDATAPAWPPGDPGTTTP-----GHSVPVPATELGSTELVTTK 177
QY 161 T 161
DB 178 T 178

RESULT 45
US-10-152-363A-60
; Sequence 60, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-60

Query Match 9.6%; Score 93; DB 14; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
QY 8 CSQNEYFDSLHACIPCOL-----RCSNTP--PLTCORYCNASVTNSVKGTHAI 56
DB 19 CVPACFDLLVRHCACGLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGL 78

Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
Db 79 FGAPALLGLALVLALVGLVSWRRRQRLRGASSAEPDGDKDAPEPL-----127
Qy 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCHFPPLPAMEGATILVTTK 160
Db 128 ---DKVII---LSPGISDATAPAWPPGDPGTTPP-----GHSVPVPATELGSTELVTTK 177
Qy 161 T 161
Db 178 T 178

RESULT 46
US-10-380-703-10
; Sequence 10, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-703-10

Query Match 9.6%; Score 93; DB 15; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSTNP--PLTCORYCNASVTSVKGTTNAIL 56
Db 19 CVPACFDLLVRHCVACGLLRTPRPKAGASSAPRTALQPQSVGAGAGEAALPLPGLL 78
Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
Db 79 FGAPALLGLALVLALVGLVSWRRRQRLRGASSAEPDGDKDAPEPL-----127
Qy 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCHFPPLPAMEGATILVTTK 160
Db 128 ---DKVII---LSPGISDATAPAWPPGDPGTTPP-----GHSVPVPATELGSTELVTTK 177
Qy 161 T 161
Db 178 T 178

RESULT 47
US-10-742-634-5
; Sequence 5, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Gaiparina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokin-alpha Complex, and Uses TH

FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-5

Query Match 9.6%; Score 93; DB 17; Length 184;
Best Local Similarity 26.5%; Pred. No. 0.33;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSTNP--PLTCORYCNASVTSVKGTTNAIL 56
Db 19 CVPACFDLLVRHCVACGLLRTPRPKAGASSAPRTALQPQSVGAGAGEAALPLPGLL 78
Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107
Db 79 FGAPALLGLALVLALVGLVSWRRRQRLRGASSAEPDGDKDAPEPL-----127
Qy 108 RTGDEIILPRGLETVVECTC-----EDCIKSKPKVDSHCHFPPLPAMEGATILVTTK 160
Db 128 ---DKVII---LSPGISDATAPAWPPGDPGTTPP-----GHSVPVPATELGSTELVTTK 177
Qy 161 T 161
Db 178 T 178

RESULT 48
US-10-380-703-7
; Sequence 7, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-703-7

Query Match 9.6%; Score 93; DB 15; Length 266;
Best Local Similarity 26.5%; Pred. No. 0.53;
Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

Qy 8 CSQNEYFDSLHACIPCOL-----RCSSTNP--PLTCORYCNASVTSVKGTTNAIL 56
Db 101 CVPACFDLLVRHCVACGLLRTPRPKAGASSAPRTALQPQSVGAGAGEAALPLPGLL 160
Qy 57 W---TCIGLSLIISLAVFLMF-----LLRKISSEPLKDFKNTGSGLLGMANIDLEKS 107

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:45:08 ; Search time 7.48624 Seconds
(without alignments)
436.984 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201

Sequence: 1 CSQNEYFDSLHACIPQLRCSNTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.79:*

2: PIR1:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 201 | 100.0 | 184 | 2 S43486 | B-cell maturation |
| 2 | 67.5 | 33.6 | 1548 | 2 S34583 | serine proteinase |
| 3 | 64.5 | 32.1 | 5376 | 2 T42215 | zonadhesin - mouse |
| 4 | 61 | 30.3 | 1101 | 2 T16840 | hypothetical prote |
| 5 | 59 | 29.4 | 1758 | 2 T15577 | hypothetical prote |
| 6 | 58 | 28.9 | 1299 | 2 T43251 | furin (EC 3.4.21.7 |
| 7 | 57.5 | 28.6 | 63 | 2 S07127 | chymotrypsin/elast |
| 8 | 57.5 | 28.6 | 1680 | 2 A43434 | furin (EC 3.4.21.7 |
| 9 | 57 | 28.4 | 1717 | 1 A45558 | epidermal growth f |
| 10 | 56 | 27.9 | 2476 | 2 T34022 | zonadhesin - pig |
| 11 | 55.5 | 27.6 | 989 | 2 T01519 | hypothetical prote |
| 12 | 55 | 27.4 | 330 | 2 T25169 | hypothetical prote |
| 13 | 55 | 27.1 | 1513 | 2 T23681 | hypothetical prote |
| 14 | 54.5 | 27.1 | 2155 | 2 T30197 | alpha tectorin - m |
| 15 | 54 | 26.9 | 1980 | 2 S54307 | myosin-heavy chain |
| 16 | 54 | 26.9 | 2022 | 2 A59256 | myosin-IXb [simila |
| 17 | 53.5 | 26.6 | 758 | 2 S46625 | finger protein IJL |
| 18 | 53 | 26.4 | 1574 | 2 T13954 | MEGF6 protein - ra |
| 19 | 53 | 26.4 | 2824 | 2 T22759 | hypothetical prote |
| 20 | 52.5 | 26.1 | 118 | 2 S61051 | hypothetical prote |
| 21 | 52 | 25.9 | 255 | 2 A84544 | hypothetical prote |
| 22 | 52 | 25.9 | 294 | 2 T23682 | hypothetical prote |
| 23 | 52 | 25.9 | 547 | 2 T34318 | hypothetical prote |
| 24 | 52 | 25.9 | 1474 | 2 D88550 | protein ZC84.6 [im |
| 25 | 52 | 25.9 | 2844 | 2 S28291 | hypothetical prote |
| 26 | 51.5 | 25.6 | 63 | 2 S57816 | antimicrobial pept |
| 27 | 51.5 | 25.6 | 282 | 2 T48763 | slah-1A protein - |
| 28 | 51.5 | 25.6 | 282 | 2 S35754 | slah-1B protein - |
| 29 | 51.5 | 25.6 | 497 | 2 T27827 | hypothetical prote |

| | | | | | | |
|-----|------|------|------|---|--------|--------------------|
| 30 | 51.5 | 25.6 | 915 | 2 | T21773 | hypothetical prote |
| 31 | 51.5 | 25.6 | 927 | 2 | T21772 | hypothetical prote |
| 32 | 51.5 | 25.6 | 999 | 2 | T19275 | hypothetical prote |
| 33 | 51.5 | 25.6 | 2120 | 2 | T30243 | alpha tectorin - c |
| 34 | 51 | 25.4 | 641 | 2 | E96612 | probable transcrip |
| 35 | 51 | 25.4 | 653 | 2 | G96675 | hypothetical prote |
| 36 | 51 | 25.4 | 746 | 2 | G84605 | hypothetical prote |
| 37 | 50.5 | 25.1 | 610 | 1 | I46001 | CAB-binding protei |
| 38 | 50 | 24.9 | 63 | 2 | S08572 | chymotrypsin/elast |
| 39 | 50 | 24.9 | 74 | 2 | S10332 | ubiquitin / riboso |
| 40 | 50 | 24.9 | 342 | 2 | T30370 | hypothetical prote |
| 41 | 50 | 24.9 | 376 | 2 | C81272 | probable aminotran |
| 42 | 50 | 24.9 | 455 | 1 | GQHUT1 | tumor necrosis fac |
| 43 | 50 | 24.9 | 561 | 2 | T27318 | hypothetical prote |
| 44 | 50 | 24.9 | 626 | 2 | T27319 | hypothetical prote |
| 45 | 50 | 24.9 | 922 | 2 | T23573 | hypothetical prote |
| 46 | 50 | 24.9 | 1360 | 2 | F96596 | hypothetical prote |
| 47 | 49.5 | 24.6 | 216 | 2 | G83398 | probable two-compo |
| 48 | 49.5 | 24.6 | 392 | 2 | T27303 | hypothetical prote |
| 49 | 49.5 | 24.6 | 1847 | 2 | T30558 | resistance protein |
| 50 | 49 | 24.4 | 189 | 2 | T48828 | hypothetical prote |
| 51 | 49 | 24.4 | 283 | 2 | C72272 | hypothetical prote |
| 52 | 49 | 24.4 | 306 | 2 | B71439 | hypothetical prote |
| 53 | 49 | 24.4 | 321 | 1 | S28390 | homeotic protein m |
| 54 | 49 | 24.4 | 346 | 2 | T20458 | hypothetical prote |
| 55 | 49 | 24.4 | 350 | 2 | JC5828 | paired-box-contain |
| 56 | 49 | 24.4 | 447 | 2 | A96639 | protein TIF3.18 [i |
| 57 | 49 | 24.4 | 461 | 2 | J44302 | tumor necrosis fac |
| 58 | 49 | 24.4 | 602 | 2 | T47794 | hypothetical prote |
| 59 | 49 | 24.4 | 654 | 2 | T30136 | hypothetical prote |
| 60 | 49 | 24.4 | 1483 | 2 | S30015 | hypothetical prote |
| 61 | 49 | 24.4 | 1620 | 2 | T27283 | hypothetical prote |
| 62 | 49 | 24.4 | 1984 | 2 | T13171 | hypothetical prote |
| 63 | 49 | 24.4 | 2531 | 2 | A46019 | probable vitelloge |
| 64 | 49 | 24.4 | 3635 | 2 | T10053 | notch-1 protein - |
| 65 | 48.5 | 24.1 | 474 | 2 | T27297 | laminin alpha 5 ch |
| 66 | 48.5 | 24.1 | 608 | 1 | ABONS1 | hypothetical prote |
| 67 | 48.5 | 24.1 | 608 | 1 | ABONS2 | serum albumin 1 pr |
| 68 | 48.5 | 24.1 | 1846 | 1 | T33079 | serum albumin 2 pr |
| 69 | 48.5 | 24.1 | 3034 | 2 | T14119 | hypothetical prote |
| 70 | 48 | 23.9 | 56 | 2 | JN0380 | seven-pass transme |
| 71 | 48 | 23.9 | 98 | 2 | C89046 | trypsin inhibitor |
| 72 | 48 | 23.9 | 304 | 1 | JC2264 | protein C10G8.4 [i |
| 73 | 48 | 23.9 | 314 | 2 | T27686 | tissue factor path |
| 74 | 48 | 23.9 | 450 | 1 | TVFVNR | hypothetical prote |
| 75 | 48 | 23.9 | 513 | 2 | D88991 | protein kinase (EC |
| 76 | 48 | 23.9 | 539 | 2 | T01513 | protein apx-1 [imp |
| 77 | 48 | 23.9 | 539 | 2 | P88188 | Crp synthase (EC 6 |
| 78 | 48 | 23.9 | 537 | 2 | T08681 | protein C18H9.7 [i |
| 79 | 48 | 23.9 | 661 | 2 | E71427 | adenosylhomocyste |
| 80 | 48 | 23.9 | 666 | 2 | T30098 | hypothetical prote |
| 81 | 48 | 23.9 | 681 | 2 | B53542 | hypothetical prote |
| 82 | 48 | 23.9 | 689 | 2 | T52060 | brefeldin A-sensit |
| 83 | 48 | 23.9 | 962 | 2 | JC5571 | protein MEDA [imp |
| 84 | 48 | 23.9 | 969 | 1 | A39490 | subtilisin-like pr |
| 85 | 48 | 23.9 | 975 | 1 | JC5570 | subtilisin-like pr |
| 86 | 48 | 23.9 | 1034 | 2 | JC5598 | subtilisin-like pr |
| 87 | 48 | 23.9 | 1079 | 1 | TVFVMI | mucin - rat |
| 88 | 48 | 23.9 | 1203 | 2 | A49175 | gag-Rml1-env polyp |
| 89 | 48 | 23.9 | 1797 | 2 | A55677 | Notch B protein - |
| 90 | 47.5 | 23.6 | 249 | 2 | T25843 | laminin beta-2 cha |
| 91 | 47.5 | 23.6 | 275 | 2 | T51437 | hypothetical prote |
| 92 | 47.5 | 23.6 | 355 | 1 | S22181 | gamma-1-microglobu |
| 93 | 47.5 | 23.6 | 546 | 2 | S67292 | probable membrane |
| 94 | 47.5 | 23.6 | 837 | 2 | S43656 | furin (EC 3.4.21.7 |
| 95 | 47.5 | 23.6 | 1188 | 2 | D86236 | protein F14N23.5 [|
| 96 | 47.5 | 23.6 | 1798 | 2 | S53869 | laminin beta-2 cha |
| 97 | 47.5 | 23.6 | 2180 | 2 | T29764 | hypothetical prote |
| 98 | 47.5 | 23.6 | 2823 | 2 | T27908 | protein T22A3.8 [i |
| 99 | 47.5 | 23.6 | 2823 | 2 | T23064 | hypothetical prote |
| 100 | 47.5 | 23.6 | 3102 | 2 | T43291 | laminin alpha chai |

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N;Alternate names: BCM protein, BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43486; S31208; S36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectional
A;Reference number: S43486; MUID:94218235; PMID:8155126
A;Accession: S43486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <LAA>
A;Cross-references: UNIPROT:Q02223; EMBL:Z29574; NID:G471244; PIDN:CAA82690.1; PID:G471244
R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(p21;p11)
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
A;Molecule type: mRNA
A;Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z14954; NID:G29407; PIDN:CAA78679.1; PID:G29408
A;Accession: S36661
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
A;Cross-references: EMBL:Z14955
C;Genetics:
A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1, 93/1
C;Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.2e-17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41
|||||
|||||

RESULT 2
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S34583
R;Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a serine proteinase
A;Reference number: S34583; MUID:93327934; PMID:8335106
A;Accession: S34583
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 <NAK>
A;Cross-references: UNIPROT:Q04592; GB:D17583; NID:G407344; PIDN:BAA04507.1; PID:d100503
C;Keywords: hydrolase; serine proteinase

Query Match 33.6%; Score 67.5; DB 2; Length 1548;
Best Local Similarity 37.8%; Pred. No. 2.4; Indels 14; Gaps 1;
Matches 14; Conservative 4; Mismatches 4

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 32
DB 1152 CAAYEWDEGSHRCQPCCHKKCRSGSPSEDQCVTCPR 1188
|||||
|||||

RESULT 3
T42215
zonadhesin - mouse
N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42215
R;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
A;Reference number: Z22080; MUID:98123114; PMID:9452463
A;Accession: T42215
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5376 <GAO>
A;Cross-references: UNIPROT:O88799; EMBL:U97068; NID:G3327420; PID:G3327421; PIDN:AAC2661
C;Genetics:
A;Gene: Zan
A;Map position: 5
C;Function:
A;Description: functions in multiple cell adhesion processes
A;Note: found exclusively on the apical region of the sperm head
C;Keywords: cell adhesion

Query Match 32.1%; Score 64.5; DB 2; Length 5376;
Best Local Similarity 35.1%; Pred. No. 16; Indels 3; Gaps 2;
Matches 13; Conservative 5; Mismatches 16

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 3300 CPTNSQFTDCLPSCVSCSNRCEVTSVPSVSCREGC 3336
|||||
|||||

RESULT 4
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
R;Geisel, C.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T10E10.
A;Reference number: Z18588
A;Accession: T16840
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:Q22378; EMBL:U39644; NID:G1049339; PID:G1049343; PIDN:AAA803
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:T10E10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 30.3%; Score 61; DB 2; Length 1101;
Best Local Similarity 37.5%; Pred. No. 11; Indels 2; Gaps 1;
Matches 12; Conservative 7; Mismatches 11

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTC 30
DB 351 CSQSTVFNSDLNVCVPLAIONSCDSSTQQPVC 382
|||||
|||||

RESULT 5
T15577
hypothetical protein C23G10.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15577
R;Latreille, P.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C23G10.
A;Reference number: Z18372

[illegible]

J. Biol. Chem. 272, 8791-8801, 1997.
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to comi
A;Reference number: Z20771; MUID: 97236843; PMID: 9079715
A;Accession: T30197
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-2155 <LEG>
A;Cross-references: UNIPROT:O08523; EMBL:X99805; NID:g1915908; PIDN:CAA68138.1; PID:g19159
A;Experimental source: strain Cbl; whole cochleae
A;Note: non-collagenous protein only expressed in the inner ear, by cells both in and su-

Query Match 27.1%; Score 54.5; DB 2; Length 2155;
Best Local Similarity 29.4%; Pred. No. 1.2e+02;
Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQOLRCSSNTPPLTCORYC 34
| | : : : | | : : : |
Db 1372 CPNSHYESCVSQCP---RCAIRLKSDCNHYC 1402

RESULT 15
S54307
myosin heavy chain - rat
C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54307
R;Reinhardt, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.
EMBO J. 14, 697-704, 1995
A;Title: A novel type of myosin implicated in signalling by rho family GTPases.
A;Reference number: S54307; MUID:95188874; PMID:7882973
A;Accession: S54307
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1980 <REI>
A;Cross-references: UNIPROT:Q63358; EMBL:X77609; NID:G639998; PIDN:CAA54700.1; PID:G6399
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z
C;Keywords: nucleotide binding; P-loop
F;149-942/Domain: myosin motor domain homology <MMOT>
F;239-246/Region: nucleotide-binding motif A (P-loop)
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 26.9%; Score 54; DB 2; Length 1980;
Best Local Similarity 52.9%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 16 PCQLRCSNTPPLTCQR 32
Db 1812 PCLLRCPDNDPLTSMK 1828

RESULT 16
A59256
myosin-IXb [similarity] - human
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59256; I61700
R;Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.
J. Cell Sci. 109, 653-661, 1996
A;Title: Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase-
A;Reference number: A59256; MUID:97063843; PMID:8907710
A;Accession: A59256
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2022 <WIR>
A;Cross-references: UNIPROT:Q14788; GB:U42391; NID:gl147782; PIDN:AAC50402.1; PID:gl1477
R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overexpression of multiple unconventional myosin gen
A;Reference number: A55758; MUID:94294418; PMID:8022818
A;Accession: I61700
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 234-322 <RES>
A;Cross-references: GB:L29149; NID:G457257; PIDN:AAA20912.1; PID:G531142
C;Genetics:
A;Gene: GDB:MYO9B; OMIM:602129
A;Map position: 19p13.1
C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C z
C;Keywords: nucleotide binding; P-loop
F;149-941/Domain: myosin motor domain homology #status atypical <MMO>
F;239-246/Region: nucleotide-binding motif A (P-loop)

Query Match 26.9%; Score 54; DB 2; Length 2022;
Best Local Similarity 52.9%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 16 PCQLRCSNTPPLTCQR 32
Db 1852 PCLLRCPDNDPLTSMK 1868

RESULT 17
S46625
finger protein YJL206c - yeast (Saccharomyces cerevisiae)
N;Alternate names: probable membrane protein YJL206c; protein J0316
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004

C;Accession: S46625; S56993
R;Purnelle, B.; Coster, F.; Goffeau, A.
Yeast 10, 1235-1249, 1994
A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifie-
ase gene ACO1 and two homologues to chromosome III genes.
A;Reference number: S46621; MUID:95274326; PMID:7754713
A;Accession: S46625
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-758 <PUR>
A;Cross-references: UNIPROT:P39529; EMBL:X77688; NID:gl183992; PIDN:CAA54752.1; PID:G547
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56977
A;Accession: S56993
A;Molecule type: DNA
A;Residues: 1-758 <PUW>
A;Cross-references: EMBL:Z49481; NID:gl015584; PIDN:CAA89502.1; PID:gl015585; MIPS:YJL20
C;Genetics:
A;Map position: 10L
C;Superfamily: GAL4 zinc binuclear cluster homology
C;Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc
F;42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 26.6%; Score 53.5; DB 2; Length 758;
Best Local Similarity 50.0%; Pred. No. 64;
Matches 11; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 13 ACIPC---QLRCSNTPPLTCQ 31
Db 46 ACIACRRKRVKRCGNTPCRLCQ 67

RESULT 18
T13954
MEGF6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:G3449293; PIDN:BA32462.1; PID:G3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

Query Match 26.4%; Score 53; DB 2; Length 1574;
Best Local Similarity 32.6%; Pred. No. 1.4e+02;
Matches 14; Conservative 6; Mismatches 13; Indels 10; Gaps 3;

Qy 1 CSQNEYFDSLHACIPCOL-----RCSSNTPPLT---CORYC 34
Db 966 CSAGAPCDVATGSGCI-CPAGRWGPRCAQSCPPLTFGLNCSQIC 1007

RESULT 19
T22759
hypothetical protein F55H12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22759
R;Dobson, R.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19610
A;Accession: T22759
A;Status: preliminary; translated from GB/EMBL/DBJ

RESULT 33

T30243

alpha tectorin - chicken

C;Species: Gallus gallus (chicken)

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T30243

R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.

Hear. Res. 130, 62-74, 1999

A;Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.

A;Reference number: 220783; MUID:99251817; PMID:10320099

A;Accession: T30243

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-2120 <COU>

A;Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:e1361092; PIDN:CAAG

A;Note: non-collagenous protein only expressed in the inner ear

Query Match 25.6%; Score 51.5; DB 2; Length 2120;

Best Local Similarity 31.4%; Pred. No. 2.7e+02;

Matches 11; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEYFDSLHACIP-CQLRCSNTPLTCQRYC 34

DB 1345 CPNSHYES-----CVSLCQPRCAAIRLKSDCGHYC 1375

RESULT 34

E96612

probable transcription factor F12K22.14 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E96612

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E96612

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-641 <STO>

A;Cross-references: UNIPROT:Q9FV33; GB:AE005173; NID:gl1079528; PIDN:AAG29238.1; GSPDB:G

C;Genetics:

A;Map position: 1

C;Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger

Query Match

Best Local Similarity 45.8%; Score 51; DB 2; Length 641;

Matches 11; Conservative 2; Mismatches 3; Indels 8; Gaps 2;

QY 15 IPCQ-----LRCSSNTPLTC 30

DB 7 LPCDGDGVCMCRKSNPPPEESLTC 30

RESULT 35

G96675

hypothetical protein T23K8.9 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G96675

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G96675

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-653 <STO>

A;Cross-references: UNIPROT:Q9S9J8; GB:AE005173; NID:g4646199; PIDN:AAD26872.1; GSPDB:GN

C;Genetics:

A;Gene: T23K8.9

A;Map position: 1

Query Match 25.4%; Score 51; DB 2; Length 653;

Best Local Similarity 42.3%; Pred. No. 1.1e+02;

Matches 11; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 7 FDSLHACIPC-----QLRCSNTPL 28

DB 204 FDEMVFHCSACNFLLDLRCVSLPPL 229

RESULT 36

G84605

hypothetical protein At2g21840 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84605

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84605

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-746 <STO>

A;Cross-references: UNIPROT:Q9SJ15; GB:AE002093; NID:g4417278; PIDN:AAD20403.1; GSPDB:GN

C;Genetics:

A;Gene: At2g21840

A;Map position: 2

Query Match

Best Local Similarity 28.6%; Score 51; DB 2; Length 746;

Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCQLRC 21

DB 267 CKETVVYDRFYLCVCECLKC 287

RESULT 37

I46001

C4b-binding protein alpha chain - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I46001; S43190

R;Hillarp, A.; Thern, A.; Dahlback, B.

J. Immunol. 153, 4190-4199, 1994

A;Title: Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains pro

A;Reference number: I46001; MUID:95015909; PMID:7930621

A;Accession: I46001

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-610 <HIL>

A;Cross-references: UNIPROT:Q28065; EMBL:Z31693; NID:g469117; PIDN:CAA83498.1; PID:g46911

C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology

F;50-107/Domain: complement factor H repeat homology <FHL>

F;112-169/Domain: complement factor H repeat homology <FH2>

A;Reference number: A60594; MUID:89171156; PMID:2924890
A;Accession: A60594
A:Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XX',60 <OLS>
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990

A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: A35010
A:Molecule type: protein
A;Residues: 41-45 <ENG>
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kiriwaka, S.; Kato, K.
Biochim. Biotechnol. Biochem. 58, 2266-2268, 1994

A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A;Reference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
A:Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F;44-83/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.9%; Score 50; DB 1; Length 455;
Best Local Similarity 35.3%; Pred. No. 1.le+02;
Matches 12; Conservative 5; Mismatches 13; Indels 4; Gaps 2;

QY 1 CSONE---YFDLSLHACIPCOLRCSSNTPELTQC 31
| | : | : | : | : | : | : |
Db 127 CRNQRYRWSENLFOCFNCSL--CLNGTVHLSCQ 159

RESULT 43
T27318 .
hypothetical protein Y69H2.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27318
R;McMurray, A.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z20343
A;Accession: T27318
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-561 <WIL>
A;Cross-references: UNIPROT:Q5ULT6; EMBL:Z98877; PIDN:CAB54472.1; GSPDB:GNO0023; CESP:Y69H2
C;Genetics:
A;Experimental source: clone Y69H2
A;Gene: CESP:Y69H2.3a
A;Map position: 5
A;Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3

Query Match 24.9%; Score 50; DB 2; Length 561;
Best Local Similarity 32.4%; Pred. No. 1.le+02;
Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;

submitted to the EMBL Data Library, January 1998
A:Reference number: Z20340
A:Accession: T27303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-392 <WIL>
A:Cross-references: UNIPROT:O9X9P6; EMBL:AL021503; PIDN:CAA16424.1; GSPDB:GN000023; CESP:
A:Experimental source: clone Y68A4A
C:Genetics:
A:Gene: CESP.Y68A4A.10

Search completed: January 28, 2005, 19:57:56
Job time : 9.48624 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 19:44:33 ; Search time 39.6147 Seconds
(without alignments)
493.825 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41

Perfect score: 201

Sequence: 1 CSQNEVDSLLHACIPQLRCSSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 201 | 100.0 | 184 | 1 | TR17_HUMAN |
| 2 | 201 | 100.0 | 184 | 2 | Q6PE36 |
| 3 | 201 | 100.0 | 184 | 2 | AAH58291 |
| 4 | 136 | 67.7 | 185 | 1 | TR17_MOUSE |
| 5 | 72.5 | 36.1 | 499 | 2 | Q88714 |
| 6 | 72.5 | 36.1 | 1674 | 2 | Q80218 |
| 7 | 72.5 | 36.1 | 2850 | 2 | Q80T03 |
| 8 | 71.5 | 35.6 | 249 | 1 | TL3X_MOUSE |
| 9 | 68.5 | 34.1 | 1569 | 2 | Q6W4X9 |
| 10 | 68.5 | 34.1 | 1569 | 2 | AAQ82434 |
| 11 | 67.5 | 33.6 | 1877 | 1 | PCK5_MOUSE |
| 12 | 66.5 | 33.1 | 293 | 1 | TL3X_HUMAN |
| 13 | 65.5 | 32.6 | 1025 | 2 | Q7R6D7 |
| 14 | 64.5 | 32.1 | 5374 | 2 | Q99ND0 |
| 15 | 64.5 | 32.1 | 5376 | 1 | ZAN_MOUSE |
| 16 | 61.5 | 30.6 | 3005 | 2 | Q6BF64 |
| 17 | 61 | 30.3 | 965 | 2 | Q22378 |
| 18 | 60 | 29.9 | 867 | 1 | SSFO_BOVIN |
| 19 | 60 | 29.9 | 5146 | 2 | Q8SPM4 |
| 20 | 59.5 | 29.6 | 353 | 2 | Q9VW81 |
| 21 | 59.5 | 29.6 | 353 | 2 | Q8Z58 |
| 22 | 59.5 | 29.6 | 581 | 2 | Q8NAV9 |
| 23 | 59.5 | 29.6 | 880 | 2 | Q8NAU9 |
| 24 | 59.5 | 29.6 | 985 | 2 | Q7Z5T8 |
| 25 | 59.5 | 29.6 | 985 | 2 | Q8IZ06 |
| 26 | 59.5 | 29.6 | 992 | 2 | Q86U29 |
| 27 | 59.5 | 29.6 | 993 | 2 | Q8IX30 |
| 28 | 59 | 29.4 | 247 | 2 | Q7Z6F5 |
| 29 | 59 | 29.4 | 937 | 2 | Q8GYR5 |
| 30 | 58 | 28.9 | 101 | 2 | Q8BR19 |
| 31 | 58 | 28.9 | 175 | 1 | TL3C_MOUSE |

| | | | | | |
|-----|------|------|------|---|------------|
| 32 | 58 | 28.9 | 175 | 2 | Q8R4W8 |
| 33 | 58 | 28.9 | 1299 | 2 | Q26489 |
| 34 | 57.5 | 28.6 | 63 | 1 | ICE1_ASCSU |
| 35 | 57.5 | 28.6 | 1679 | 1 | FUR2_DROME |
| 36 | 57 | 28.4 | 321 | 2 | Q9MAA0 |
| 37 | 57 | 28.4 | 1210 | 2 | Q7R165 |
| 38 | 57 | 28.4 | 1717 | 2 | Q26566 |
| 39 | 56.5 | 28.1 | 1476 | 2 | Q8WRP4 |
| 40 | 56 | 27.9 | 341 | 2 | Q6P233 |
| 41 | 56 | 27.9 | 341 | 2 | Q8CPA7 |
| 42 | 56 | 27.9 | 341 | 2 | Q9D351 |
| 43 | 56 | 27.9 | 341 | 2 | AAH64748 |
| 44 | 56 | 27.9 | 387 | 2 | Q9PVD4 |
| 45 | 56 | 27.9 | 392 | 2 | Q6NUF1 |
| 46 | 56 | 27.9 | 392 | 2 | AAH68640 |
| 47 | 56 | 27.9 | 2476 | 1 | ZAN_PIG |
| 48 | 55.5 | 27.6 | 146 | 2 | Q9EP28 |
| 49 | 55.5 | 27.6 | 225 | 2 | Q9V240 |
| 50 | 55.5 | 27.6 | 673 | 2 | Q86WK8 |
| 51 | 55.5 | 27.6 | 955 | 2 | Q96DN2 |
| 52 | 55.5 | 27.6 | 989 | 2 | Q9ZU00 |
| 53 | 55.5 | 27.6 | 1084 | 2 | Q6IRM7 |
| 54 | 55.5 | 27.6 | 1084 | 2 | AAH70831 |
| 55 | 55.5 | 27.6 | 2898 | 2 | Q9VLT6 |
| 56 | 55 | 27.4 | 147 | 1 | MSRB_VIBPA |
| 57 | 55 | 27.4 | 330 | 2 | O18118 |
| 58 | 55 | 27.4 | 344 | 2 | Q924K7 |
| 59 | 55 | 27.4 | 663 | 2 | Q81YJ8 |
| 60 | 55 | 27.4 | 686 | 2 | Q6POM3 |
| 61 | 55 | 27.4 | 686 | 2 | AAH65554 |
| 62 | 55 | 27.4 | 724 | 2 | Q6BUV7 |
| 63 | 55 | 27.4 | 858 | 1 | TTC7_HUMAN |
| 64 | 55 | 27.4 | 1073 | 2 | Q6QI57 |
| 65 | 55 | 27.4 | 1073 | 2 | AAH66242 |
| 66 | 55 | 27.4 | 1074 | 2 | Q964D1 |
| 67 | 55 | 27.4 | 1101 | 2 | Q964D2 |
| 68 | 55 | 27.4 | 1127 | 2 | Q993K9 |
| 69 | 55 | 27.4 | 1513 | 2 | O17970 |
| 70 | 54.5 | 27.1 | 146 | 2 | Q9EP23 |
| 71 | 54.5 | 27.1 | 752 | 2 | Q9C091 |
| 72 | 54.5 | 27.1 | 1792 | 2 | O57484 |
| 73 | 54.5 | 27.1 | 2155 | 1 | TECA_HUMAN |
| 74 | 54.5 | 27.1 | 2155 | 1 | TECA_MOUSE |
| 75 | 54 | 26.9 | 89 | 1 | VPI_MESMA |
| 76 | 54 | 26.9 | 501 | 2 | Q8WVD2 |
| 77 | 54 | 26.9 | 695 | 2 | Q93539 |
| 78 | 54 | 26.9 | 718 | 2 | Q9BI07 |
| 79 | 54 | 26.9 | 1980 | 1 | MY9B_RAT |
| 80 | 54 | 26.9 | 2114 | 1 | MY9B_MOUSE |
| 81 | 54 | 26.9 | 2158 | 1 | MY9B_HUMAN |
| 82 | 54 | 26.9 | 2447 | 2 | Q9NEF9 |
| 83 | 54 | 26.9 | 3215 | 2 | Q8IRV7 |
| 84 | 54 | 26.9 | 4117 | 2 | Q8IRV9 |
| 85 | 54 | 26.9 | 4179 | 2 | Q9W4Y4 |
| 86 | 54 | 26.9 | 4223 | 2 | Q8MRN3 |
| 87 | 54 | 26.9 | 4228 | 2 | Q8IRV8 |
| 88 | 53.5 | 26.6 | 146 | 2 | Q9EP09 |
| 89 | 53.5 | 26.6 | 246 | 2 | Q9TUX4 |
| 90 | 53.5 | 26.6 | 281 | 2 | Q29475 |
| 91 | 53.5 | 26.6 | 285 | 2 | Q95326 |
| 92 | 53.5 | 26.6 | 290 | 2 | Q7Q883 |
| 93 | 53.5 | 26.6 | 381 | 1 | P53_CANFA |
| 94 | 53.5 | 26.6 | 414 | 2 | Q68813 |
| 95 | 53.5 | 26.6 | 758 | 1 | YJU6_YEAST |
| 96 | 53.5 | 26.6 | 1069 | 2 | Q9BP52 |
| 97 | 53.5 | 26.6 | 2843 | 2 | Q9Y6R7 |
| 98 | 53.5 | 26.6 | 3084 | 2 | Q7RSL8 |
| 99 | 53 | 26.4 | 131 | 1 | ALK1_MOUSE |
| 100 | 53 | 26.4 | 131 | 2 | AAO09307 |

ALIGNMENTS


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FT VARIANT 75 75 /FTid=VAR_018756.
FT FT -> V.
FT VARIANT 81 81 /FTid=VAR_018757.
FT FT S -> N.
FT VARIANT 153 153 /FTid=VAR_018758.
FT FT A -> T.
FT VARIANT 165 165 /FTid=VAR_012234.
FT FT C -> S.
SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 201; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
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Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 2
Q6PE46 PRELIMINARY; PRT; 184 AA.
AC Q6PE46;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 17.
GN Name=TNFRSF17;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058291; AAH58291.1; -.
KW Receptor.
SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;

Query Match 100.0%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
|||||
Db 8 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 4
TR17_MOUSE STANDARD; PRT; 185 AA.
AC O88472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell
DE maturation protein).
GN Name=TNFRSF17; Synonyms=BCMA, BCM;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

```


gel-forming mucin gene cluster between human and mouse.";

RT
RL Genomics 81:433-436(2003).
DR ENBL; AY184388; AAO47735.1;
DR ENBL; AY184385; AAO47735.1; JOINED.
DR ENBL; AY184387; AAO47735.1; JOINED.
DR ENBL; AY184386; AAO47735.1; JOINED.
DR HSPF; O46162; IKJ0.
DR MGD; MGI:12663233; Muc6.
DR InterPro; IPR002919; Cysrich TIL.
DR InterPro; IPR006207; Cys knot C.
DR InterPro; IPR009041; PMP_SGCI.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK 2; 1.
SQ SEQUENCE 2850 AA; 300398 MW; 9CD95F0845C79C9D CRC64;

Query Match 36.1%; Score 72.5; DB 2; Length 2850;
Best Local Similarity 48.3%; Pred. No. 2.3;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 1 CSQNEYFDSLHACIPCQLRCSSNTPTLT 29
||| ||||| ||| |||
Db 1222 CSQNEYFDHSEGTGVCP-----APPTT 1243

RESULT 8

T13X_MOUSE

ID_T13X_MOUSE STANDARD; PRT; 249 AA.

AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=Tnftrsf13b; Synonyms=Taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for BlyS demonstrates a crucial role in
RT humoral immunity";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRATN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354693; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmmond S., Gustinchich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglath D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varadar R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayata N.,


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Qy 1 CSQNEYFDLSLHACIPCOLRCSSNTPPLTQRYC 34
Db 6 CPKPDQWSSRSKSCVSCALTCSQRS-QRTCTDFC 38

RESULT 9
Q6W4X9 PRELIMINARY; PRT; 1569 AA.
AC Q6W4X9;
AC 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Mucin glycoprotein (Fragment).
GN Name=MUC6;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RX PubMed=15081123;
RX Rouseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,
RA Toribara N.W.;
RT "The complete genomic organization of the human MUC6 and MUC2 mucin
RT genes.";
RL Genomics 83:936-939(2004).
DR EMBL; AY312160; AAQ82434.1; --
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR009041; FMP_SGCI.
DR InterPro; IPR006552; VMC_out.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 2.
DR Pfam; PF00094; VWD; 3.
DR SMART; SM00215; VMC_out; 2.
DR SMART; SM00216; VWD; 3.
DR NON_TER 1569
FT SEQUENCE 1569 AA; 168065 MW; 6AEDEE143ECB855B CRC64;
SQ

Query Match 34.1%; Score 68.5; DB 2; Length 1569;
Best Local Similarity 45.2%; Pred. No. 4.1;
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gap

Qy 1 CSQNEYFDLSLHACIPCOLRCSSNTPPLTQ 31
Db 1179 CSQDEYFDHERGVGVPCV-----PPTTPQ 1202

RESULT 10
AAQ82434 PRELIMINARY; PRT; 1569 AA.
ID AAQ82434
AC AAQ82434;
AC 23-APR-2004 (TReMBLrel. 27, Created)
DT 23-APR-2004 (TReMBLrel. 27, Last sequence update)
DT 23-APR-2004 (TReMBLrel. 27, Last annotation update)
DE Mucin glycoprotein (Fragment).
GN Name=MUC6.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RX PubMed=15081123;
RX Rouseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,
RA Toribara N.W.;
RT "The complete genomic organization of the human MUC6 and MUC2 mucin
RT genes.";
RL Genomics 83:936-939(2004).
DR EMBL; AY312160; AAQ82434.1; --
DR NON_TER 1569
FT SEQUENCE 1569 AA; 168065 MW; 6AEDEE143ECB855B CRC64;
SQ

```

Query Match 34.1%; Score 68.5; DB 2; Length 1569;
 Best Local Similarity 45.2%; Pred.No. 4.1;
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 1 CSQNEYPDSLLHACIPQCLRCSSNTPPLTCQ 31
 DB_ 1179 CSQNEYPDSLLHACIPQCLRCSSNTPPLTCQ 1202

RESULT 11

ID_PCK5 MOUSE STANDARD; PRT; 1877 AA.

AC Q04592; Q02040; PRT; 1877 AA.

DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)

DE (Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)

DE (Subtilisin-like proprotein convertase 6) (SPC6).

GN Name=PC5K5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).

RC STRAIN=ICR; TISSUE=Intestine;

RX MEDLINE=93327934; PubMed=8335106;

RA Nakagawa T., Murakami K., Nakayama K.;

RT "Identification of an isoform with an extremely large Cys-rich region
 of PC5, a Kex2-like processing endoprotease.";

RL FEBS Lett. 327:165-171 (1993).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Brain, and Intestine;

RX MEDLINE=93224489; PubMed=8468318;

RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 Nakayama K.;

RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACE4.";

RL J. Biochem. 113:132-135 (1993).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM PC5A).

RC TISSUE=Adrenal cortex;

RX MEDLINE=93342056; PubMed=8341687;

RA Lussan J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;

RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).

RN [4]

RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.

RX MEDLINE=97103178; PubMed=8947550;

RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 Bendaian M., Seidah N.G.;

RT "The isoforms of proprotein convertase PC5 are sorted to different
 subcellular compartments.";

RL J. Cell Biol. 135:1261-1275 (1996).

RN [5]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=96293359; PubMed=8698813;

RA Constam D.B., Calton M., Robertson E.J.;

RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";

RL J. Cell Biol. 134:181-191 (1996).

RN [6]

RP DEVELOPMENTAL EXPRESSION.

RX MEDLINE=97436919; PubMed=8291583;

RA Rancourt S.L., Rancourt D.E.;

RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";

RL Dev. Genet. 21:75-81 (1997).

CC -!- FUNCTION: Likely to represent a widespread endoprotease activity
 within the constitutive and regulated secretory pathway. Capable
 of cleavage at the RX(K/R)R consensus motif. May be responsible
 for the maturation of gastrointestinal peptides. May be involved
 in the cellular proliferation of adrenal cortex via the activation
 of growth factors.

CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
 propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 can be any amino acid and Yaa is Arg or Lys.

CC -!- SUBCELLULAR LOCATION: PC5A is secreted through the regulated
 secretory pathway. PC5B is a type I membrane protein localized to
 a paranuclear post-Golgi network compartment in communication with
 early endosomes.

CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=PC5B; Synonyms=Long;
 IsoId=Q04592-1; Sequence=Displayed;
 Name=PC5A; Synonyms=Short;

CC -!- TISSUE SPECIFICITY: PC5A is expressed in most tissues but is most
 abundant in the intestine and adrenals. PC5B is expressed in the
 intestine, adrenals and lung but not in the brain.

CC -!- DEVELOPMENTAL STAGES: Weakly expressed throughout the embryo,
 except in the developing nervous system, the ribs and the liver,
 but markedly up-regulated at discrete sites during development. At
 E6.5, prominent expression observed in differentiated decidua. At
 E7.5, intense expression in extraembryonic endoderm, amnion and
 nascent mesoderm. At E8.5, abundant expression in somites and yolk
 sac followed by a confinement to dermamyotome compartment. Between
 E9.5 and E11.5, abundant expression in AER (thickened ectodermal
 cells of limb buds). At E12.5, expression in the limbs is confined
 to the condensing mesenchym surrounding the cartilage. At this
 stage, strong expression also detected in vertebral and facial
 cartilage primordia and in the muscle of the tongue. At E16.5,
 abundant expression in epithelial cells of the intestinal villi.
 Isoform A is most abundant at all stages but significant levels of
 isoform B occur at E12.5.

CC -!- DOMAIN: The propeptide domain acts as an intramolecular chaperone
 assisting the folding of the zymogen within the endoplasmic
 reticulum.

CC -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain
 sorting information. AC 1 directs TGN localization and interacts
 with the TGN sorting protein PACS-1.

CC -!- SIMILARITY: Belongs to peptidase family S8.

CC -!- SIMILARITY: Contains 1 homo B/P domain.

CC -----

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CC -----

CC EMBL; D17583; BAA04507.1; -;
 EMBL; D12619; BAA02143.1; -;
 EMBL; L14932; AAA74636.1; -;
 PIR; A48225; A48225
 PIR; S34583; S34583
 HSP; P23188; IP8J.
 MEROPS; S08.076; -;
 MD; MG1.97515; Pcsk5.
 InterPro; IPR006211; Furin-like.
 InterPro; IPR009030; Grow_fac_recept.
 InterPro; IPR011031; MultThaem_cyt.
 InterPro; IPR000209; Pept_S8_S53.
 InterPro; IPR002884; Prptcnconvertsp.
 Pfam; PF00757; Furin-like; 2.
 Pfam; PF00082; Peptidase S8; 1.
 Pfam; PF01483; P_protein; 1.
 PRINTS; PR00723; SUBTILISIN.

QY 1 CSQNEYFDSLLHACIP-COLRCSSNTP--PLTCQRYC 34
 Db 3298 CPTNSQFTDCLPSCVPCSNRCVTSVPSSCREG 3334

RESULT 15

ZAN MOUSE
 ID ZAN MOUSE STANDARD; PRT: 5376 AA.
 AC O88799; O08647;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Zonadhesin precursor.
 GN Name=Zan;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98123114; PubMed=9452463;
 RA Gao Z., Garbers D.L.;
 RT "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like domains.";
 RT J. Biol. Chem. 273:3415-3421(1998).
 RL [2]
 RP SEQUENCE OF 4864-5376 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97271566; PubMed=9126492;
 RA Gao Z., Harumi T., Garbers D.L.;
 RT "Chromosome localization of the mouse zonadhesin gene and the human zonadhesin gene (ZAN).";
 RL Genomics 41:119-122(1997).
 CC -!- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling.
 CC -!- SUBUNIT: Probably forms covalent oligomers.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head.
 CC -!- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.
 CC -!- DOMAIN: The NAM domains probably mediates sperm adhesion to the zona pellucida.
 CC -!- DOMAIN: During sperm migration through the reproductive tracts, the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.
 CC -!- DOMAIN: The VWFD domain 2 may mediate covalent oligomerization (By similarity).
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 3 NAM domains.
 CC -!- SIMILARITY: Contains 25 VWFD domains.
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 EMBL; U97068; AAC26680.1; -;
 EMBL; U83190; AAC53125.1; -;
 PIR; T42215; T42215;
 HSSP; Q90248; 1HX2.
 MGD; MGI:106656; Zan.
 InterPro; IPR002919; Cysrich_TIL.
 InterPro; IPR000742; EGF_2.
 InterPro; IPR006209; EGF_like.
 InterPro; IPR000998; NAM.
 InterPro; IPR003328; TILA Cysrich.
 InterPro; IPR001846; VWF_D.

DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00629; NAM; 3.
 DR Pfam; PF01826; TIL; 25.
 DR Pfam; PF02345; TIL_assoc; 25.
 DR Pfam; PF00094; VWF; 4.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 18.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00740; NAM_1; FALSE_NEG.
 DR PROSITE; PS00060; NAM_2; 3.
 KW Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 5376 Zonadhesin.
 FT DOMAIN 18 5310 Extracellular (Potential).
 FT TRANSEM 5311 5337 Potential.
 FT DOMAIN 5338 5376 Cytoplasmic (Potential).
 FT DOMAIN 45 210 MAM 1.
 FT DOMAIN 215 374 MAM 2.
 FT DOMAIN 377 542 MAM 3.
 FT DOMAIN 547 1170 80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
 (MUCIN-LIKE DOMAIN).
 FT DOMAIN 1171 1280 VWFD 1 (partial).
 FT DOMAIN 1281 1669 VWFD 2.
 FT DOMAIN 1670 2056 VWFD 3.
 FT DOMAIN 2057 2459 VWFD 4.
 FT DOMAIN 2460 2579 VWFD 5 (partial).
 FT DOMAIN 2580 2699 VWFD 6 (partial).
 FT DOMAIN 2700 2819 VWFD 7 (partial).
 FT DOMAIN 2820 2939 VWFD 8 (partial).
 FT DOMAIN 2940 3059 VWFD 9 (partial).
 FT DOMAIN 3060 3179 VWFD 10 (partial).
 FT DOMAIN 3180 3299 VWFD 11 (partial).
 FT DOMAIN 3300 3416 VWFD 12 (partial).
 FT DOMAIN 3417 3536 VWFD 13 (partial).
 FT DOMAIN 3537 3656 VWFD 14 (partial).
 FT DOMAIN 3657 3776 VWFD 15 (partial).
 FT DOMAIN 3777 3892 VWFD 16 (partial).
 FT DOMAIN 3893 4928 VWFD 17 (partial).
 FT DOMAIN 4029 4148 VWFD 18 (partial).
 FT DOMAIN 4149 4263 VWFD 19 (partial).
 FT DOMAIN 4264 4283 VWFD 20 (partial).
 FT DOMAIN 4384 4503 VWFD 21 (partial).
 FT DOMAIN 4504 4623 VWFD 22 (partial).
 FT DOMAIN 4624 4743 VWFD 23 (partial).
 FT DOMAIN 4744 4863 VWFD 24 (partial).
 FT DOMAIN 4864 5261 VWFD 25.
 FT DOMAIN 5259 5295 EGF-like.
 FT DISULFID 5263 5274 By similarity.
 FT DISULFID 5268 5283 By similarity.
 FT DISULFID 5285 5294 By similarity.
 FT CARBOHYD 339 339 N-linked (GlcNAc...)
 FT CARBOHYD 499 499 N-linked (GlcNAc...)
 FT CARBOHYD 1216 1216 N-linked (GlcNAc...)
 FT CARBOHYD 1239 1239 N-linked (GlcNAc...)
 FT CARBOHYD 1314 1314 N-linked (GlcNAc...)
 FT CARBOHYD 1814 1814 N-linked (GlcNAc...)
 FT CARBOHYD 1908 1908 N-linked (GlcNAc...)
 FT CARBOHYD 1933 1933 N-linked (GlcNAc...)
 FT CARBOHYD 2028 2028 N-linked (GlcNAc...)
 FT CARBOHYD 2111 2111 N-linked (GlcNAc...)
 FT CARBOHYD 2142 2142 N-linked (GlcNAc...)
 FT CARBOHYD 2332 2332 N-linked (GlcNAc...)
 FT CARBOHYD 2533 2533 N-linked (GlcNAc...)
 FT CARBOHYD 2575 2575 N-linked (GlcNAc...)
 FT CARBOHYD 2692 2692 N-linked (GlcNAc...)
 FT CARBOHYD 2812 2812 N-linked (GlcNAc...)
 FT CARBOHYD 3052 3052 N-linked (GlcNAc...)
 FT CARBOHYD 3065 3065 N-linked (GlcNAc...)
 FT CARBOHYD 3144 3144 N-linked (GlcNAc...)
 FT CARBOHYD 3172 3172 N-linked (GlcNAc...)
 FT CARBOHYD 3288 3288 N-linked (GlcNAc...)
 FT CARBOHYD 3292 3292 N-linked (GlcNAc...)

FT CARBOHYD 3782 3782 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4005 4005 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4136 4136 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4243 4243 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4254 4254 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4335 4335 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4376 4376 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 4586 4586 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 5136 5136 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 5252 5252 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 5376 AA; 579908 MW; 0E44DB7DF2A2620 CRC64;

Query Match 32.1%; Score 64.5; DB 1; Length 5376;
 Best Local Similarity 35.1%; Pred. No. 50;
 Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIP-CQLRCSNTP--PLTCQRYC 34
 Db 3300 CPTNSQFTDCLPSCVPSCNCEVTSPSPVSCREGC 3336

RESULT 16

Q6BFG4 PRELIMINARY; PRT; 3005 AA.
 AC Q6BFG4;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative surface protein with EGF domains and furin-like repeats.
 GN ORFNames=PTMB.409;
 OS Paramecium tetraurelia.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramecium.
 OX NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Stock d4-2;
 RA Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
 RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
 RA Cohen J., Meyer E., Sperling L.;
 RT "High coding density on the largest Paramecium tetraurelia somatic
 RT chromosome."
 RL Curr. Biol. 0:0-0(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Stock d4-2;
 RA Zagulski M., Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
 RA Nowak J.K., Migdalski A., Gromadka R., Nowacki M., Migdalski A.,
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR548612; CAH03606.1; -;
 SQ SEQUENCE 3005 AA; 343821 MW; D8CC6A247876A5A5 CRC64;

Query Match 30.6%; Score 61.5; DB 2; Length 3005;
 Best Local Similarity 40.6%; Pred. No. 68;
 Matches 13; Conservative 3; Mismatches 7; Indels 9; Gaps 2;

Qy 6 YFDSLHACIP-CQLRCSNTPPLTCQ---RYC 34
 Db 1190 YFESSTNQICDLSC-----FTCGSSKYC 1215

RESULT 17

Q22378 PRELIMINARY; PRT; 966 AA.
 ID Q22378;
 AC Q22378;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein T10E10.4.
 GN ORFNames=T10E10.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Geisel C.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U39644; AAA80360.2; -;
 DR PIR; T16840; T16840.
 DR HSSP; P10969; LWGT.
 DR WormPep; T10E10.4; CE25989.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008061; P:chitin binding; IEA.
 DR GO; GO:0006030; P:chitin metabolism; IEA.
 DR InterPro; IPR002557; Chitin_bind_Pera.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR003571; Snake toxin.
 DR InterPro; IPR006150; Worm_repeat_1.
 DR Pfam; PF01607; CBM_14; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00289; WRI; 12.
 DR PROSITE; PS00606; B_KETOACYL SYNTHASE; UNKNOWN_1.
 DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;

Query Match 30.3%; Score 61; DB 2; Length 966;
 Best Local Similarity 37.5%; Pred. No. 24;
 Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIP-CQLR--CSSNTPPLTC 30
 Db 216 CSQSTVFNSDLNVCVPLAIQNSCDSDSTQQPVC 247

RESULT 18

SSPO_BOVIN STANDARD; PRT; 867 AA.
 ID SSPO_BOVIN
 AC P98167;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE SCO-spondin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ependymocyte;
 RX MEDLINE=96338614; PubMed=8743952;
 RA Gobron S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
 RA Lamalle D., Dastugue B., Meinzel A.;
 RT "SCO-spondin: a new member of the thrombospondin family secreted by
 RT the subcommissural organ is a candidate in the modulation of neuronal

RT aggregation.";

RL J. Cell Sci. 109:1053-1061(1996).

CC -!- FUNCTION: Involved in the modulation of neuronal aggregation.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: Subcommissural organ.

CC -!- DEVELOPMENTAL STAGE: Embryo.

CC -!- SIMILARITY: Belongs to the thrombospondin family.

CC -!- SIMILARITY: Contains at least 2 EGF-like domains.

CC -!- SIMILARITY: Contains at least 1 F5/8 type C domain.

CC -!- SIMILARITY: Contains at least 3 LDL-receptor class A domains.

CC -!- SIMILARITY: Contains at least 4 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 VWFC domain.

CC -----

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CC -----

DR EMBL; X93922; CAA63815.1; --

DR HSP; P01130; LAJU

DR InterPro; IPR002919; Cysrich_TIL.

DR InterPro; IPR000421; FAS8_C.

DR InterPro; IPR008979; Gal_Bind_like.

DR InterPro; IPR002172; LDL_receptor_A.

DR InterPro; IPR009041; PMP_SGCI.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP_1.

DR InterPro; IPR001007; VWFC_C.

DR Pfam; PF00754; F5_F8_type_C_1.

DR Pfam; PF00057; Ldl_recept_a; 3.

DR Pfam; PF01826; TIL; 1.

DR Pfam; PF00090; TSP_1; 4.

DR Pfam; PF00093; VWFC_1.

DR PRINTS; PRO0261; LDLRECEPTOR.

DR PRINTS; PRO1705; TSP1REPEAT.

DR PROSITE; PS01285; FAS8C_1; 1.

DR PROSITE; PS01286; FAS8C_2; 1.

DR PROSITE; PS00022; FAS8C_3; 1.

DR PROSITE; PS01209; LDLRA_1; 3.

DR PROSITE; PS00068; LDLRA_2; 3.

DR PROSITE; PS00092; TSP1; 4.

DR PROSITE; PS0184; VWFC_2; 1.

DR Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.

FT NON_TER 1

FT DOMAIN 1

FT DOMAIN 29 87 TSP type-1 1.

FT DOMAIN 103 142 EGF-like 1.

FT DOMAIN 143 180 EGF-like 2.

FT DOMAIN 188 244 TSP type-1 2.

FT DOMAIN 245 304 VWFC.

FT DOMAIN 344 502 F5/8 type C.

FT DOMAIN 506 544 LDL-receptor class A 1.

FT DOMAIN 663 701 LDL-receptor class A 2.

FT DOMAIN 723 761 LDL-receptor class A 3.

FT DOMAIN 761 814 TSP type-1 3.

FT DOMAIN 816 866 TSP type-1 4.

FT DISULFID 107 122 By similarity.

FT DISULFID 116 127 By similarity.

FT DISULFID 129 141 By similarity.

FT DISULFID 147 166 By similarity.

FT DISULFID 149 169 By similarity.

FT DISULFID 171 179 By similarity.

FT DISULFID 344 502 By similarity.

FT DISULFID 508 520 By similarity.

FT DISULFID 515 533 By similarity.

FT DISULFID 527 542 By similarity.

FT DISULFID 665 677 By similarity.

FT DISULFID 672 690 By similarity.

FT DISULFID 684 699 By similarity.

FT DISULFID 725 737 By similarity.

FT DISULFID 732 750 By similarity.

FT DISULFID 744 759 By similarity.

FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 409 409 N-linked (GlcNAc...) (Potential).

FT NON_TER 867 867

SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;

Query Match 29, 98; Score 60; DB 1; Length 867;

Best Local Similarity 42.98; Pred. No. 29;

Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 10 LHACIPCOLRCSSNTPLTC 30

Db 96 VFHACVPCPLTCDDISGOATC 116

RESULT 19

Q8SPM4 PRELIMINARY; PRT; 5146 AA.

AC Q8SPM4;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE SCO-spondin.

GN Name=sco-spondin;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Subcommissural organ;

RX MEDLINE=20465125; PubMed=11008217;

RA Gobron S.;

RT "Subcommissural organ/Reissner's fiber complex: characterization of

RT SCO-spondin, a glycoprotein with potent activity on neurite

RT outgrowth.";

RL Glia 32:177-191(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Subcommissural organ;

RA Meintzel A.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ416457; CAC94914.1; --

DR HSP; P98162; IK7B

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR GO; GO:0030414; F:protease inhibitor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR002919; Cysrich_TIL.

DR InterPro; IPR006207; Cys_knot_C.

DR InterPro; IPR011489; EMI.

DR InterPro; IPR000421; FAS8_C.

DR InterPro; IPR001545; Gly_hormone8.

DR InterPro; IPR002172; LDL_receptor_A.

DR InterPro; IPR009041; PMP_SGCI.

DR InterPro; IPR008037; ProE_inh_PMP.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR001007; VWFC_C.

DR InterPro; IPR001846; VWFC_D.

DR Pfam; PF07546; EMI; 1.

DR Pfam; PF00754; F5_F8_type_C; 1.

DR Pfam; PF00057; Ldl_recept_a; 10.

DR Pfam; PF05375; Pacifastin_I; 1.

DR Pfam; PF01826; TIL; 10.

DR Pfam; PF00090; TSP_1; 25.

DR Pfam; PF00093; VWC; 1.

DR Pfam; PF00094; VWD; 3.

DR PRINTS; PRO0261; LDLRECEPTOR.

DR SMART; SM00041; CT; 1.

DR SMART; SM00231; FAS8C; 1.

DR SMART; SM00068; GHF; 1.

| | |
|----|--|
| DR | SMART; SMO0192; LDla; 10. |
| DR | SMART; SMO0209; TSPI; 25. |
| DR | SMART; SMO0214; WVC; 3. |
| DR | SMART; SMO0216; VWD; 3. |
| DR | PROSITE; PS01225; CTCK_2; 1. |
| DR | PROSITE; PS01285; FA58C_1; UNKNOWN_1. |
| DR | PROSITE; PS01286; FA58C_2; 1. |
| DR | PROSITE; PS00222; FA58C_3; 1. |
| DR | PROSITE; PS00261; GLYCO HORMONE_BETA_1; 2. |
| DR | PROSITE; PS01209; LDLRA_1; 7. |
| DR | PROSITE; PS00068; LDLRA_2; 9. |
| DR | PROSITE; PS00092; TSPI_25. |
| DR | PROSITE; PS01208; VWFC_1; UNKNOWN_1. |
| DR | PROSITE; PS01084; VWFC_2; 2. |
| SQ | SEQUENCE 5146 AA; 543588 MW; 724CSFB8727E13DA CRC64; |

| | | | | |
|-----------------------|-------|-------------------|-------|---------------------------------|
| Query Match | 29.9% | Score 60; | DB 2; | Length 5146; |
| Best Local Similarity | 42.9% | Pred No. 1.9e+02; | | |
| Matches | 9; | Conservative | 3; | Mismatches 9; Indels 0; Gaps 0; |

| | | |
|----|------|----------------------------|
| QY | 10 | LLHACIPCOLRCCSSNTPTLTC 30 |
| | : | ::::: |
| Db | 1814 | VFHACVPCPLTCDDISGQATC 1834 |

| |
|--|
| RESULT 20 |
| Q9VM81 |
| ID Q9VM81 PRELIMINARY; PRT; 353 AA. |
| AC Q9VM81 AC |
| DT 01-MAY-2000 (TREMBLrel. 13, Created) |
| DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) |
| DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) |
| DE CG7348-PA. |
| GN ORFNames=CG7348; |
| OS Drosophila melanogaster (Fruit fly). |
| OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; |
| OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; |
| OC Ephydroidea; Drosophilidae; Drosophila. |
| NCBI_TaxID=7227; |
| [1] |
| SEQUENCE FROM N.A. |
| MDLINE=2019606; PubMed=10731132; |
| Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., |
| Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., |
| George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N., |
| Sutton G.G., Mortman J.R., Vandell M.D., Zhang Q., Chen L.X., |
| Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D., |
| Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., |
| Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., |
| Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M., |
| Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., |
| Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P., |
| Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., |
| Cherry J.M., Clawley S., Dahlke C., Davenport L.B., Davies P., |
| de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., |
| Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., |
| Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W., |
| Roesler K., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., |
| Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., |
| Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., |
| Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C., |
| Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., |
| Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., |
| Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., |
| Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., |
| Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., |
| Neou S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., |
| Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., |
| Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., |
| Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., |
| Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., |
| Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., |
| Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., |

Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Saeki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Nat. Genet. 36:40-45(2004).
DR ENBL; AK092010; BAC03789.1; -.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDALB4EE1 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 581;
Best Local Similarity 28.9%; Pred. No. 22;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps

QY 1 CSQNEYFDSLLHACTPCOI-----RCSSWT 25
|||:::||||:
DB 337 CSPGHYNTSIHRCAMGYSQPDFRNFRCSPCGNT 374

RESULT 23

QNA9U9 PRELIMINARY; PRT; 880 AA.

AC QNA9U9; 22, Last sequence update)
ID QNA9U9; 22, Last sequence update)
AD QNA9U9; 26, Last annotation update)
IC QNA9U9; 26, Last annotation update)
DE Hypothetical protein FLJ34743.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX NCBI
RP SEQUENCE FROM N.A.
RZ PubMed=14702039;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura T., Irie H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Horuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Sacoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Saeki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

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"Complete sequencing and characterization of 21,243 full-length human
cDNAs.",
NA. Genet. 36:40-45 (2004).
EMBL; AK092062; BAC03798.1; -.
HSSP; P35555; 1LMJ.
Genew; HGNC:13655; CEGF3.
GO; GO:0016020; C-membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004888; P:transmembrane receptor activity; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000859; CUB_1.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_CA.
InterPro; IPR006209; EGF-like.
InterPro; IPR009030; Grow fac recept.
InterPro; IPR001491; Thrbomoduln.
Pfam; PF00431; CUB; 1.
Pfam; PF00008; EGF; 4.
Pfam; PF07645; EGF_CA; 2.
PRINTS; PR00907; THRBMODULN.
SMART; SM0042; CUB; 1.
SMART; SM00179; EGF_CA; 3.
PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS00026; EGF_3; 3.
PROSITE; PS01187; EGF_CA; 3.
EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 880 AA; 97239 MW; FOBDSE85266FD60 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 880;
Best Local Similarity 28.9%; Pred. No. 34;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOL-----RCSSNT 25
Db 636 CSPGHYNTSIHRCICAMGSYQDFRQNFCSRCPGNT 673

RESULT 24
QZ75T8 PRELIMINARY; PRT; 985 AA.
AC QZ75T8
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC26979.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
[1]

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC054338; AAH54338.1; -.
DR InterPro; IPR000150; Hypothet cof.
DR PROSITE; PS01228; COF_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 985 AA; 110858 MW; 71109F095C12E89 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 985;
Best Local Similarity 21.6%; Pred. No. 39;
Matches 11; Conservative
Qy 1 CSQNEYFDSLHACIPC-----QLRCSSNTPPTQCR 32
Db 39 CDNNQYFDISALSCVPCGANQRQDARGTSCVCLPFGQMISNNGGPAICKK 89

RESULT 25
Q8IZ06 PRELIMINARY; PRT; 985 AA.
AC Q8IZ06;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC26979 protein.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC032835; AAH32835.1; -.
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR000150; Hypothet cof.
DR PROSITE; PS01228; COF_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 985 AA; 110872 MW; 971B5626C726B3B4 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 985;

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Best Local Similarity 28.9%; Pred. No. 39;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDLLHACIPCQL-----RCSNNT 25
  |||  |||  |||  |||  |||  |||  |||
Db 748 CSPGHYYNTSIHRCICAMGSYOPDPFRNFCRCPCGNT 785

```

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RESULT 27
Q8IX30
ID Q8IX30 PRELIMINARY; PRT; 993 AA.
AC Q8IX30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CUB and EGF containing protein.
DE DE Name=CEGF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP Pfart N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R.,
RA Hankeln T., Winterpacht A.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF452494; AAN76808.1; -.
DR HSSP; P35555; IEMN.
GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000859; CUB_2.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 4.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00266; EGF_3; 5.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 993 AA; 109282 MW; 19BBE0E5627EEAF4 CRC64;

Query Match          29.6%; Score 59.5; DB 2; Length 993;
Best Local Similarity 28.9%; Pred.No. 39;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY      1 CSQNEYFDLSLLHACIPCOL-----RCSNST 25
       |||:::|||||||:
Db     749 CSPGHGYNTSIHRCICAMGSYQPDFRQNFCSRCPGNT 786
               |||:::|||||||:

RESULT 28
Q7Z6F5
ID Q7Z6F5 PRELIMINARY; PRT; 247 AA.
AC Q7Z6F5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane activator and CAML interactor.
DE DE Name=TNFRSF1B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RA
```


RA SEQUENCE FROM N.A.
RP Mizuno K., Irie S., Sato T.-A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350257; AAL83914.1; -;
DR HSSP; Q96RJ3; 1QOE.
DR MGI; MGI:1919299; Tnfrsf13c.
SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EB93B1 CRC64;

Query Match 28.9%; Score 58; DB 2; Length 175;
Best Local Similarity 47.4%; Pred. No. 10;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOL 19
Db 22 CNOQTECPDLVRNCVCEL 40

RESULT 33

Q26489 PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=SF9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S8.
DR EMBL; Z69888; CAA93116.1; -;
DR PIR; T43251; T43251.
DR HSSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.
DR InterPro; IPR00345; CytC heme BS.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR009030; Grow Fac. recept.
DR InterPro; IPR011031; Multihem. cyt.
DR InterPro; IPR000209; Pept. S8_S53.
DR InterPro; IPR009020; Prot. inh. propept.
DR InterPro; IPR002884; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF01483; P:proteolysis; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00190; CVTCHROME C; UNKNOWN 3.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 1299 AA; 142019 MW; 4C3799C7B8C572AB CRC64;

Query Match 28.9%; Score 58; DB 2; Length 1299;
Best Local Similarity 37.1%; Pred. No. 82;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps 2;

Qy 1 CSQNEYFDSLHACIPCOLRCS-----SNTPLPLTC 30
Db 1150 CSRPLRIDRLNQCVCPC---CSERGVTNSTPTTDC 1181

RESULT 34

ICEL_ASCSU STANDARD; PRT; 63 AA.
AC P07851; O77419;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Chymotrypsin/elastase isoform 1 (C/E-1 inhibitor) (ASC/E-1).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN 1;
RP SEQUENCE.
RX MEDLINE=84255715; PubMed=6564898;
RA Babin D.R., Peanasky R.J., Goos S.M.;
RT "The isoform of chymotrypsin/elastase from Ascaris lumbricoidea:
the primary structure.";
RL Arch. Biochem. Biophys. 232:143-161(1984).
RN 2;
RP SEQUENCE FROM N.A.
RX MEDLINE=98297373; PubMed=9635450;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RT "Anieakis simplex: mutational bursts in the reactive site centers of
serine protease inhibitors from an ascarid nematode.";
RL Exp. Parasitol. 89:257-261(1998).
RN 3;
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
RX MEDLINE=95006335; PubMed=7922044;
RA Huang K., Strynadka N.C., Bernard V.D., Peanasky R.J., James M.N.;
RT "The molecular structure of the complex of Ascaris
chymotrypsin/elastase inhibitor with porcine elastase.";
RL Structure 2:679-689(1994).
CC -1- FUNCTION: Defends the organism against the host's proteinases.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
EMBL; U94499; AAC61300.1; -;
PDB; 1EAI; X-ray; C/D=1-61.
DR InterPro; IPR002919; Cysrich_TIL.
DR Pfam; PF01826; TIL; 1.
KW 3D-structure; Direct protein sequencing; Serine protease inhibitor.
FT DOMAIN 5 60 TIL.
FT SITE 31 32 Reactive bond.
FT DISULFID 5 38
FT DISULFID 14 33
FT DISULFID 17 29
FT DISULFID 21 60
FT DISULFID 40 54
FT CONFLICT 4 4 S -> R (in Ref. 2).
FT CONFLICT 23 24 PD -> DP (in Ref. 2).
FT TURN 3 4
FT TURN 7 8
FT STRAND 10 12
FT STRAND 15 15
FT STRAND 20 20
FT TURN 25 26
FT STRAND 28 30
FT STRAND 34 34
FT STRAND 37 39

FT HELIX 42 44
 FT TURN 45 45
 FT STRAND 46 48
 FT TURN 50 51
 FT STRAND 54 56
 FT HELIX 57 59
 SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;

Query Match 28.6%; Score 57.5; DB 1; Length 63;
 Best Local Similarity 37.1%; Pred. No. 4.1;
 Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

Qy 1 CSQNEYFDLHACIPCLRC--SSNTP-PLTCOR 32
 ||| : : : : : ||| : : : : :
 5 CGPNEVWTE----CTGCEMKCGPDENTCPLMCR 35

Db

RESULT 35

FUR2 DROME
 ID FUR2 DROME STANDARD; PRT; 1679 AA.
 AC P30432; Q24301; Q8S2S2;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
 GN Name=Fur2; ORFNames=CGI8734;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

SEQUENCE FROM N.A. (ISOFORM D).
 RC STRAIN=Oregon-R, Tuebingen, and Iso-1;
 RX MEDLINE=92381036; PubMed=1512259;
 RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
 RA Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
 RT "Cloning and functional expression of Dfurin2, a subtilisin-like
 RT proprotein processing enzyme of Drosophila melanogaster with multiple
 RT repeats of a cysteine motif";
 RL J. Biol. Chem. 267:17208-17215(1992).
 RN [2]

SEQUENCE FROM N.A. (ISOFORM D).
 RC STRAIN=ISO-1;
 RX MEDLINE=95186060; PubMed=7880443;
 RA Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
 RA van de Ven W.J.M.;
 RT "The Dfur2 gene of Drosophila melanogaster: Genetic organization,
 RT expression during embryogenesis, and pro-protein processing activity
 RT of its translational product Dfurin2";
 RL DNA Cell Biol. 14:223-234(1995).
 RN [3]

SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burbis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhou X., Zhou S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster";
 Science 287:2185-2195(2000).
 RL [4]

REVISIONS, AND ALTERNATIVE SPLICING.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]

SEQUENCE OF 305-1679 FROM N.A. (ISOFORM A).
 RC STRAIN=Berkley; TISSUE=Embryo;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -I- FUNCTION: Furin is likely to represent the ubiquitous endoprotease
 CC activity within constitutive secretory pathways and capable of
 CC cleavage at the RX(K/R)R consensus motif (By similarity).
 CC -I- CATALYTIC ACTIVITY: Release of mature proteins from their
 CC propeptides by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa
 CC can be any amino acid and Yaa is Arg or Lys. Releases albumin,
 CC complement component C3 and von Willebrand factor from their
 CC respective precursors.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=D; Synonyms=E;
 CC IsoId=P30432-1; Sequence=Displayed;
 CC Name=A; Synonyms=B;
 CC IsoId=P30432-2; Sequence=VSP_009365;
 CC Note=No experimental confirmation available;
 CC -I- TISSUE SPECIFICITY: transient expression in a subset of central
 CC nervous system neurons during embryonic stages 12-13. Expression
 CC in developing tracheal tree from stage 13 to end of embryonic
 CC development.
 CC -I- SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
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 CC -----
 CC EMBL; M94375; AAA28551.1; -.

DR EMBL; L33831; AAA69860.1; --;
 DR EMBL; AB003502; AAF48598.2; --;
 DR EMBL; AB003502; AAN09400.1; --;
 DR EMBL; AY070553; AAL48024.1; ALT_INIT.
 DR PIR; A43434; A43434.
 DR HSSP; P23188; 1P8J.
 DR MEROPS; S08.049; --;
 DR FlyBase; FBgn0004598; Fur2.
 DR GO; GO:0004276; F:furin activity; IDA.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR011031; Multihem_cyt..
 DR InterPro; IPR000209; Pept_S8_S53.
 DR InterPro; IPR009020; Prot_inh_propept.
 DR InterPro; IPR002884; Pprtnconvertsp.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR Pfam; PF01483; P_protein; 2.
 DR PRINTS; PD00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 DR Repeat; PS00138; SUBTILASE_SER; 1.
 KW Alternative splicing; Glycoprotein; Hydrolase; Multigene family;
 KW Repeat; Serine protease; Signal; Transmembrane; Zymogen.
 FT SIGNAL 1 ? Potential.
 FT PROPEP 318 Potential.
 FT CHAIN 319 1679 Furin-like protease 2.
 FT ACT_SITE 417 417 Charge relay system (By similarity).
 FT ACT_SITE 456 456 Charge relay system (By similarity).
 FT ACT_SITE 637 637 Charge relay system (By similarity).
 FT DOMAIN 961 1443 10 X tandem repeats, Cys-rich.
 FT REPEAT 961 1006 1.
 FT REPEAT 1007 1056 2.
 FT REPEAT 1057 1103 3.
 FT REPEAT 1104 1152 4.
 FT REPEAT 1153 1204 5.
 FT REPEAT 1205 1253 6.
 FT REPEAT 1254 1298 7.
 FT REPEAT 1299 1345 8.
 FT REPEAT 1346 1392 9.
 FT REPEAT 1393 1443 10.
 FT TRANSMEM 1512 1532 Potential.
 FT DOMAIN 1533 1679 Cytoplasmic (Potential).
 FT DISULFID 473 629 By similarity.
 FT DISULFID 565 595 By similarity.
 FT DISULFID 720 748 By similarity.
 FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 442 442 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 927 927 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1060 1060 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1181 1181 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1274 1274 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1277 1277 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1439 1439 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 386 386 L -> LVSK (in isoform A).
 FT FTID-VSP 009365.
 FT MISSING (in Ref. 1).
 FT CONFLICT 152 153 Missing (in Ref. 1).
 FT CONFLICT 177 177 V -> F (in Ref. 1).
 FT CONFLICT 213 213 V -> VDQL (in Ref. 1).
 SQ SEQUENCE 1679 AA; 183369 MW; 3F9E749F0B021CF6 CRC64;
 Query Match 28.6%; Score 57.5; DB 1; Length 1679;
 Best Local Similarity 34.3%; Pred. No. 1.2e+02;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLCRSS-NTPEPLTCQRYC 34
 Db 1198 CSESEFYQVEGQCRPCHASGCSNGPADTSC 1232
 RESULT 36
 Q9MAM0 PRELIMINARY; PRT; 321 AA.
 AC Q9MAM0
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T25K16.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OK NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
 RA Theologis A., Ecker J.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
 RA Ecker J.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 Myb-like domain.
 DR EMBL; AC007323; AAF26467.1; --;
 DR HSSP; P54274; IITY.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR011011; FYVE PHD ZnF.
 DR InterPro; IPR009057; Homeodomain like.
 DR InterPro; IPR001005; Myb_DNA_binding.
 DR InterPro; IPR001965; ZnF_PHD.
 DR SMART; SM00717; SANT; 1.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS50090; MYB_3; 1.
 DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
 KW Nuclear protein.
 SQ SEQUENCE 321 AA; 36643 MW; F3411A75DBC0B406 CRC64;
 Query Match 28.4%; Score 57; DB 2; Length 321;
 Best Local Similarity 41.4%; Pred. No. 26;
 Matches 12; Conservative 1; Mismatches 10; Indels 6; Gaps 1;
 Qy 12 HACIPQLR-----CSSNTPPLTCQRYC 34
 Db 63 HAGIVCDIADGGVVPVCSGNECLAVHRKC 91
 RESULT 37
 Q7RL65 PRELIMINARY; PRT; 1210 AA.
 AC Q7RL65
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLP_447_61408_57776.

DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF01030; Recep_L domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00261; FU; 6.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 2.
DR PROSITE; PS00119; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00028; ZINC FINGER C2H2.1; UNKNOWN 1.
KW Kinase; Receptor; Signal; Transferase; Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1717 epidermal growth factor receptor.
SQ SEQUENCE 1717 AA; 192303 MW; 1101A338C1653D8C CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1717;
Best Local Similarity 40.9%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 11; Indels 0;

QY 1 CSONEYFDSLHACIPQLRCS 22
| : | | | | : | | | | |
DB 646 CPRTYIDPQTRHCLPCNESCS 667

RESULT 39
ID QSWRF4 PRELIMINARY; PRT; 1476 AA.
AC QSWRF4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Receptor tyrosine kinase.
DE DEceptor tyrosine kinase.
GN Name=MBRTK1;
OS Monosiga brevicollis.
OC Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.
OX NCBI_TaxID=81824;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50154;
RA MEDLINE=21625102; PubMed=11752452;
RX King N., Carroll S.B.
RT "A receptor tyrosine kinase from choanoflagellates: molecular
RT into early animal evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 98:15032-15037(2001).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50154;
RX MEDLINE=22752268; PubMed=12869759;
RA King N., Hittiger C.T., Carroll S.B.
RT "Evolution of key cell signaling and adhesion protein families
RT predates animal origins."
RL Science 301:361-363(2003).
RX ENBL; AF401359; AAL33602.2; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004672; F:receptor activity; IEA.
DR GO; GO:0006486; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF07645; EGF_Ca; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00084; Sushi; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SMO0355; ZnF_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
SQ SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred.No. 37;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSQNEYFDLSILHACIPQLRCSSNTPEPLTCQRVC 34
|::||::|::|::|::|::|::|::|:
DB 60 CNEREWESQLIRSLPHEGVRCPSQLAPIPFQNYC 93

RESULT 41
Q8CFA7 PRELIMINARY; PRT; 341 AA.

ID Q8CFA7
AC Q8CFA7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Germ cell specific zinc finger protein.
GN Name=Zfp393; Synonyms=Gzf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV x C57BL; TISSUE=Testis;
RX MEDLINE=22239718; PubMed=12351194;
RA Yan W., Burns K.H., Ma L., Matzuk M.M.;
RT "Identification of Zfp393, a germ cell-specific gene encoding a novel
RT zinc finger protein.";
RL Mech. Dev. 118:233-239 (2002).
DR ENBL; AF508984; AAN31656.1; -.
DR HSSP; P08047; ISP1.
DR MGD; MG1:2181068; Zfp393.
DR GO; GO:007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SMO0355; ZnF_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
SQ SEQUENCE 341 AA; 38073 MW; AC82D4C0472B054C CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred.No. 37;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSQNEYFDLSILHACIPQLRCSSNTPEPLTCQRVC 34
|::||::|::|::|::|::|::|::|:
DB 60 CNEREWESQLIRSLPHEGVRCPSQLAPIPFQNYC 93

RESULT 42
Q9D351 PRELIMINARY; PRT; 341 AA.

ID Q9D351
AC Q9D351;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus in vitro fertilized eggs cDNA, RIKEN full-length enriched
DE library, clone/7420700M5 product:weakly similar to DJ67568.1 (NOVEL
DE ZINC FINGER PROTEIN).
GN Name=7420700M5Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
  Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multipipette sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
  Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
  Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
  Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
  Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
  Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
  Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
  Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
  Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
  Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
  Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK018361; BAB31177.1; -.
DR HSPG; P08047; ISPL.
DR MGD; MG11923003; 7420700M05Rik.
DR GO; GO:0007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF000096; zf-C2H2; 3.
DR ProDom; PD000003; Znf C2H2; 2.
DR SMART; SM00335; Znf C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
SQ SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFFC CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred. No. 37;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
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QY 1 CSN09YFDSLHACIPQLRCSSNTPTLCQYVC 34
Db 60 CNERWESQILRSLPHEGVRCPSQLAPIPFQNYC 93

RESULT 43
AAH64748
ID AAH64748 PRELIMINARY; PRT; 341 AA.
AC AAH64748;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Zinc finger protein 393.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
  Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
  Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
  Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064748; AAH64748.1; -.
SQ SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred. No. 37;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
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QY 1 CSN09YFDSLHACIPQLRCSSNTPTLCQYVC 34
Db 60 CNERWESQILRSLPHEGVRCPSQLAPIPFQNYC 93

RESULT 44
Q9PVD4
ID Q9PVD4 PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P75-like transmembrane protein fullback.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
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RP SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF131890; AAD54072.1; -.
DR HSP; P0174; INGR.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR000488; DEATH.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 27.9%; Score 56; DB 2; Length 387;
Best Local Similarity 25.4%; Pred. No. 42;
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;

QY 1 CSQNEYFDSLHACIPCOL-----RC-----SSNTPPLTQC 31
Db 103 CPERQYLDLS-NGICLPQLCSKGHVVSQCTHNKNTVCQLCSSGFYSEVKSSESPLPCR 161
QY 32 RYC 34
Db 162 TEC 164

RESULT 45
Q6NUF1
ID Q6NUF1 PRELIMINARY; PRT; 392 AA.
AC Q6NUF1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE LOC398134 protein (Fragment).
GN Xenus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC068640; AAH68640.1; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
FT NON_TER 1
SQ SEQUENCE 392 AA; 42538 MW; 0B41CED6CCE080FB CRC64;

Query Match 27.9%; Score 56; DB 2; Length 392;
Best Local Similarity 25.4%; Pred. No. 43;
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;

QY 1 CSQNEYFDSLHACIPCOL-----RC-----SSNTPPLTQC 31
Db 108 CPERQYLDLS-NGICLPQLCSKGHVVSQCTHNKNTVCQLCSSGFYSEVKSSESPLPCR 165
QY 32 RYC 34
Db 167 TEC 169

RESULT 46
AAH68640
ID AAH68640 PRELIMINARY; PRT; 392 AA.
AC AAH68640;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE LOC398134 protein (Fragment).
GN LOC398134.
OS Xenus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068640; AAH68640.1; -;
FT NON TER 1
SQ SEQUENCE 392 AA; 42538 MW; 0B41CED6CCE080FB CRC64;
Query Match 27.9%; Score 56; DB 2; Length 392;
Best Local Similarity 25.4%; Pred. NO. 43;
Matches 16; Conservative 6; Mismatches 11; Indels 30; Gaps 3;
QY 1 CSONEYFSLHACIPCOL-----RC-----SSNTPPLTCQ 31
Db 108 CPERQYLDN-NGICLLPCLCSKGHVVSQCTHNKNTVCQLCSSGFYSEKVSSESFCPLPCR 166
QY 32 RYC 34
Db 167 TEC 169
RESULT 47
ZAN_PIG STANDARD; PRT; 2476 AA.
AC Q28983;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Zonadhesin precursor.
GN Name=ZAN;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;
RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
RP 1658-1667; 1777-1795 AND 1914-1921.
RC STRAIN=Meishan; TISSUE=Testis;
RA MEDLINE=96064658; PubMed=7592795;
RA Hardy D.M., Garbers D.L.;
RT "A sperm membrane protein that binds in a species-specific manner to
RT the egg extracellular matrix is homologous to von Willebrand factor.";
RL J. Biol. Chem. 270:26025-26028(1995).
CC -1- FUNCTION: Binds in a species-specific manner to the zona pellucida
CC of the egg. May be involved in gamete recognition and/or
CC signaling.
CC -1- SUBUNIT: Probably forms covalent oligomers.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the
CC apical region of the sperm head (By similarity).
CC -1- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.
CC -1- NOT IN lung, liver, heart, spleen, brain, kidney, epididymis.
CC -1- DOMAIN: The MAM domains probably mediate sperm adhesion to the
CC zona pellucida.
CC -1- DOMAIN: During sperm migration through the reproductive tracts,
CC the mucin-like domain might inhibit inappropriate trapping of
CC spermatozoa or promoting adhesion to the oviductal isthmus.
CC -1- DOMAIN: The VWFD domains 2 and 3 may mediate covalent

oligomerization (By similarity to human intestinal mucin MUC2).
-1- PTM: The MAM domains and the mucin-like domains are missing from
the zonadhesin that binds to the egg extracellular matrix.
Processing might occur during sperm maturation and/or
capacitation.
-1- SIMILARITY: Contains 1 EGF-like domain.
-1- SIMILARITY: Contains 2 MAM domains.
-1- SIMILARITY: Contains 5 VWFD domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U40024; AAC48486.1; -;
CC PIR; T34022; T34022.
DR HGSP; Q90248; IHX2.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR003328; TILA_Cysrich.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00629; MAM; 2.
DR Pfam; PF01826; TIL; 5.
DR Pfam; PF02345; TIL_assoc; 5.
DR Pfam; PF00094; VWD; 4.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00214; VWC; 2.
DR SMART; SM00216; VWD; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00600; MAM_2; 2.
KW Cell adhesion; Direct protein sequencing; EGF-like domain;
KW Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 29
FT CHAIN 30 2476
FT Zonadhesin.
FT DOMAIN 30 2418
FT Extracellular (Potential).
FT TRANSMEM 2419 2439
FT Potential.
FT DOMAIN 2440 2476
FT Cytoplasmic (Potential).
FT DOMAIN 31 144
FT MAM 1.
FT DOMAIN 147 312
FT MAM 2.
FT DOMAIN 319 687
FT 53 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
FT (MUCIN-LIKE DOMAIN).
FT VWFD 1 (partial).
FT DOMAIN 688 799
FT VWFD 2.
FT DOMAIN 800 1184
FT VWFD 3.
FT DOMAIN 1185 1573
FT VWFD 4.
FT DOMAIN 1574 1968
FT VWFD 5.
FT DOMAIN 1969 2370
FT EGF-like.
FT DOMAIN 2366 2402
FT DISULFID 2370 2381
FT By similarity.
FT DISULFID 2375 2390
FT By similarity.
FT DISULFID 2392 2401
FT By similarity.
FT CARBOHYD 109 109
FT N-linked (GlcNAc...)
FT CARBOHYD 269 269
FT N-linked (GlcNAc...)
FT CARBOHYD 735 735
FT N-linked (GlcNAc...)
FT CARBOHYD 758 758
FT N-linked (GlcNAc...)
FT CARBOHYD 833 833
FT N-linked (GlcNAc...)
FT CARBOHYD 1154 1154
FT N-linked (GlcNAc...)
FT CARBOHYD 1329 1329
FT N-linked (GlcNAc...)
FT CARBOHYD 1448 1448
FT N-linked (GlcNAc...)
FT CARBOHYD 1544 1544
FT N-linked (GlcNAc...)
FT CARBOHYD 1596 1596
FT N-linked (GlcNAc...)
FT CARBOHYD 1654 1654
FT N-linked (GlcNAc...)

FT CARBOHYD 1843 1843 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1965 1965 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2122 2122 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2165 2165 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2178 2178 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2329 2329 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 2359 2359 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 823 823 C -> V (in Ref. 1; AA sequence).
 FT CONFLICT 923 923 S -> Y (in Ref. 1; AA sequence).
 FT CONFLICT 965 965 W -> Y (in Ref. 1; AA sequence).
 FT CONFLICT 1241 1241 S -> K (in Ref. 1; AA sequence).
 SQ SEQUENCE 2476 AA; 270364 MW; A13B690375A6548C CRC64;

Query Match 27.9%; Score 56; DB 1; Length 2476;
 Best Local Similarity 31.6%; Pred. No. 2.9e+02;
 Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 1 CSQNEYFDLSLHACIP-CQ---LRCSNTPPLTCQRYC 34
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 1851 CSAHSVYTSVPSCLPSCQDPGEGCTGAGAPSTCEEGC 1888

RESULT 48

Q9EP28 PRELIMINARY; PRT; 146 AA.
 AC Q9EP28;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Polypeptide (fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinzawa H., Shao L., Jiang Q., Togashi H., Zhang X., Iehibashi M.,
 RA Watanabe H., Saito T., Takahashi T., Ohba K., Mizokami M.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030968; BAB11770.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR002519; HCV env.
 DR Pfam; PF01539; HCV env; I.
 KW Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON TER 1 1
 FT NON TER 146 146
 SQ SEQUENCE 146 AA; 15763 MW; 9C67046FD8507C30 CRC64;

Query Match 27.6%; Score 55.5; DB 2; Length 146;
 Best Local Similarity 31.8%; Pred. No. 18;
 Matches 14; Conservative 6; Mismatches 13; Indels 11; Gaps 3;

Qy 1 CSQN----EYFDSLH--ACIPCO-----LRCSNTPPLTCQRY 33
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 34 CSNNSITWLTDAVHLHFGVPCPSDNGTLRCWQVTPNAVY 77

RESULT 49

Q9VE40 PRELIMINARY; PRT; 225 AA.
 AC Q9VE40;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CG714-PA (RH24988p).
 GN ORFNames=CG714;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Balswin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
 RA Nelson D.B., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomes perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

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OM protein - protein search, using sw model

Run on: January 28, 2005, 19:36:38 ; Search time 9.04587 Seconds
(without alignments)
249.264 Million cell updates/sec

Title: US-10-077-137-1_COPY_8_41
Perfect score: 201
Sequence: 1 CSQNEVFDLLHACIPQLRCSNTPPLTCQRYC 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCOTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 201 | 100.0 | 34 | 4 | US-09-854-864-7 |
| 2 | 201 | 100.0 | 51 | 4 | US-09-854-864-6 |
| 3 | 201 | 100.0 | 58 | 4 | US-09-854-864-21 |
| 4 | 201 | 100.0 | 81 | 4 | US-09-854-864-13 |
| 5 | 201 | 100.0 | 181 | 4 | US-09-854-864-5 |
| 6 | 201 | 100.0 | 184 | 4 | US-09-854-864-11 |
| 7 | 201 | 100.0 | 283 | 4 | US-09-854-864-9 |
| 8 | 136 | 67.7 | 185 | 4 | US-09-854-864-17 |
| 9 | 136 | 67.7 | 185 | 4 | US-09-854-864-11 |
| 10 | 136 | 67.7 | 281 | 4 | US-09-854-864-10 |
| 11 | 93.5 | 46.5 | 117 | 4 | US-09-854-864-12 |
| 12 | 66.5 | 33.1 | 59 | 4 | US-09-854-864-20 |
| 13 | 66.5 | 33.1 | 67 | 4 | US-09-854-864-16 |
| 14 | 66.5 | 33.1 | 166 | 2 | US-08-810-572A-6 |
| 15 | 66.5 | 33.1 | 166 | 3 | US-09-290-333-6 |
| 16 | 66.5 | 33.1 | 166 | 4 | US-09-782-857A-6 |
| 17 | 66.5 | 33.1 | 166 | 4 | US-09-854-864-15 |
| 18 | 66.5 | 33.1 | 293 | 2 | US-08-810-572A-2 |
| 19 | 66.5 | 33.1 | 293 | 3 | US-09-290-333-2 |
| 20 | 66.5 | 33.1 | 293 | 4 | US-09-782-857A-2 |
| 21 | 66.5 | 33.1 | 293 | 4 | US-09-879-519-22 |
| 22 | 66.5 | 33.1 | 293 | 4 | US-09-848-295-4 |
| 23 | 66.5 | 33.1 | 293 | 4 | US-09-854-864-14 |
| 24 | 66.5 | 33.1 | 397 | 4 | US-09-854-864-18 |
| 25 | 56 | 27.9 | 2476 | 2 | US-08-276-967-2 |
| 26 | 54 | 26.9 | 98 | 4 | US-09-621-976-6330 |
| 27 | 54 | 26.9 | 431 | 4 | US-09-252-991A-25721 |

| | | | | | | |
|-----|------|------|------|---|-------------------|--------------------|
| 28 | 53.5 | 26.6 | 381 | 3 | US-09-257-580-2 | Sequence 2, Appli |
| 29 | 53.5 | 26.6 | 5405 | 3 | US-08-718-388-9 | Sequence 9, Appli |
| 30 | 52.5 | 26.1 | 142 | 4 | US-09-848-295-2 | Sequence 2, Appli |
| 31 | 52 | 25.9 | 547 | 4 | US-09-877-730-26 | Sequence 26, Appli |
| 32 | 52 | 25.9 | 624 | 4 | US-09-877-730-24 | Sequence 24, Appli |
| 33 | 52 | 25.9 | 712 | 4 | US-09-877-730-22 | Sequence 22, Appli |
| 34 | 52 | 25.9 | 826 | 4 | US-09-877-730-16 | Sequence 16, Appli |
| 35 | 52 | 25.9 | 904 | 4 | US-09-877-730-6 | Sequence 6, Appli |
| 36 | 52 | 25.9 | 991 | 4 | US-09-877-730-12 | Sequence 12, Appli |
| 37 | 52 | 25.9 | 1069 | 4 | US-09-877-730-2 | Sequence 2, Appli |
| 38 | 51.5 | 25.6 | 63 | 1 | US-08-117-080-12 | Sequence 12, Appli |
| 39 | 51.5 | 25.6 | 63 | 1 | US-08-471-329-12 | Sequence 12, Appli |
| 40 | 51.5 | 25.6 | 63 | 2 | US-08-915-142-12 | Sequence 4, Appli |
| 41 | 51.5 | 25.6 | 77 | 2 | US-08-465-380-4 | Sequence 40, Appli |
| 42 | 51.5 | 25.6 | 77 | 2 | US-08-465-380-40 | Sequence 33, Appli |
| 43 | 51.5 | 25.6 | 77 | 2 | US-08-480-478-33 | Sequence 4, Appli |
| 44 | 51.5 | 25.6 | 77 | 2 | US-08-486-397-4 | Sequence 40, Appli |
| 45 | 51.5 | 25.6 | 77 | 2 | US-08-486-397-40 | Sequence 4, Appli |
| 46 | 51.5 | 25.6 | 77 | 2 | US-08-486-399-4 | Sequence 40, Appli |
| 47 | 51.5 | 25.6 | 77 | 2 | US-08-486-399-40 | Sequence 4, Appli |
| 48 | 51.5 | 25.6 | 77 | 2 | US-08-461-965-4 | Sequence 40, Appli |
| 49 | 51.5 | 25.6 | 77 | 2 | US-08-461-965-40 | Sequence 33, Appli |
| 50 | 51.5 | 25.6 | 77 | 2 | US-08-326-110A-33 | Sequence 4, Appli |
| 51 | 51.5 | 25.6 | 77 | 2 | US-08-634-641-4 | Sequence 40, Appli |
| 52 | 51.5 | 25.6 | 77 | 2 | US-08-634-641-40 | Sequence 4, Appli |
| 53 | 51.5 | 25.6 | 77 | 3 | US-09-249-471-4 | Sequence 40, Appli |
| 54 | 51.5 | 25.6 | 77 | 3 | US-09-249-471-40 | Sequence 4, Appli |
| 55 | 51.5 | 25.6 | 77 | 3 | US-09-249-472-4 | Sequence 40, Appli |
| 56 | 51.5 | 25.6 | 77 | 3 | US-09-249-472-40 | Sequence 4, Appli |
| 57 | 51.5 | 25.6 | 77 | 3 | US-09-249-451-4 | Sequence 40, Appli |
| 58 | 51.5 | 25.6 | 77 | 3 | US-09-249-451-40 | Sequence 4, Appli |
| 59 | 51.5 | 25.6 | 77 | 3 | US-08-809-455-4 | Sequence 40, Appli |
| 60 | 51.5 | 25.6 | 77 | 3 | US-08-809-455-40 | Sequence 4, Appli |
| 61 | 51.5 | 25.6 | 77 | 3 | US-09-249-461-4 | Sequence 40, Appli |
| 62 | 51.5 | 25.6 | 77 | 3 | US-09-249-461-40 | Sequence 4, Appli |
| 63 | 51.5 | 25.6 | 77 | 3 | US-09-249-448-4 | Sequence 40, Appli |
| 64 | 51.5 | 25.6 | 77 | 3 | US-09-249-448-40 | Sequence 4, Appli |
| 65 | 51.5 | 25.6 | 77 | 4 | US-09-249-473-4 | Sequence 40, Appli |
| 66 | 51.5 | 25.6 | 77 | 4 | US-09-249-473-40 | Sequence 36, Appli |
| 67 | 51.5 | 25.6 | 81 | 2 | US-08-465-380-7 | Sequence 7, Appli |
| 68 | 51.5 | 25.6 | 81 | 2 | US-08-480-478-36 | Sequence 36, Appli |
| 69 | 51.5 | 25.6 | 81 | 2 | US-08-486-397-7 | Sequence 7, Appli |
| 70 | 51.5 | 25.6 | 81 | 2 | US-08-486-399-7 | Sequence 7, Appli |
| 71 | 51.5 | 25.6 | 81 | 2 | US-08-461-965-7 | Sequence 36, Appli |
| 72 | 51.5 | 25.6 | 81 | 2 | US-08-326-110A-36 | Sequence 7, Appli |
| 73 | 51.5 | 25.6 | 81 | 2 | US-08-634-641-7 | Sequence 7, Appli |
| 74 | 51.5 | 25.6 | 81 | 3 | US-09-249-471-7 | Sequence 7, Appli |
| 75 | 51.5 | 25.6 | 81 | 3 | US-09-249-472-7 | Sequence 7, Appli |
| 76 | 51.5 | 25.6 | 81 | 3 | US-09-249-451-7 | Sequence 7, Appli |
| 77 | 51.5 | 25.6 | 81 | 3 | US-08-809-455-7 | Sequence 7, Appli |
| 78 | 51.5 | 25.6 | 81 | 3 | US-09-249-461-7 | Sequence 7, Appli |
| 79 | 51.5 | 25.6 | 81 | 3 | US-09-249-448-7 | Sequence 7, Appli |
| 80 | 51.5 | 25.6 | 81 | 4 | US-09-249-473-7 | Sequence 20, Appli |
| 81 | 51.5 | 25.6 | 100 | 2 | US-08-465-380-20 | Sequence 48, Appli |
| 82 | 51.5 | 25.6 | 100 | 2 | US-08-480-478-48 | Sequence 20, Appli |
| 83 | 51.5 | 25.6 | 100 | 2 | US-08-486-397-20 | Sequence 20, Appli |
| 84 | 51.5 | 25.6 | 100 | 2 | US-08-486-399-20 | Sequence 20, Appli |
| 85 | 51.5 | 25.6 | 100 | 2 | US-08-461-965-20 | Sequence 20, Appli |
| 86 | 51.5 | 25.6 | 100 | 2 | US-08-326-110A-48 | Sequence 20, Appli |
| 87 | 51.5 | 25.6 | 100 | 2 | US-08-634-641-20 | Sequence 20, Appli |
| 88 | 51.5 | 25.6 | 100 | 3 | US-09-249-471-20 | Sequence 20, Appli |
| 89 | 51.5 | 25.6 | 100 | 3 | US-09-249-472-20 | Sequence 20, Appli |
| 90 | 51.5 | 25.6 | 100 | 3 | US-09-249-451-20 | Sequence 20, Appli |
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| 92 | 51.5 | 25.6 | 100 | 3 | US-08-249-461-20 | Sequence 20, Appli |
| 93 | 51.5 | 25.6 | 100 | 3 | US-09-249-448-20 | Sequence 20, Appli |
| 94 | 51.5 | 25.6 | 100 | 4 | US-09-249-473-20 | Sequence 81, Appli |
| 95 | 51.5 | 25.6 | 192 | 1 | US-08-086-428B-81 | Sequence 81, Appli |
| 96 | 51.5 | 25.6 | 192 | 2 | US-08-468-570-81 | Sequence 81, Appli |
| 97 | 51.5 | 25.6 | 192 | 2 | US-08-290-665A-81 | Sequence 81, Appli |
| 98 | 51.5 | 25.6 | 192 | 4 | US-08-466-601A-81 | Sequence 81, Appli |
| 99 | 51.5 | 25.6 | 192 | 5 | PCT-US95-10398-81 | Sequence 12, Appli |
| 100 | 51.5 | 25.6 | 282 | 4 | US-09-544-618-12 | |

ALIGNMENTS

```
RESULT 1
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      100.0%; Score 201; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 2
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match      100.0%; Score 201; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db      5 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 38

RESULT 3
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      100.0%; Score 201; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 4
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      100.0%; Score 201; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
Db      1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34

RESULT 5
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      100.0%; Score 201; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 5 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 38

RESULT 6
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 8 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 41

RESULT 7
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match      100.0%; Score 201; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 5 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 38

RESULT 8
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17

Query Match      67.7%; Score 136; DB 4; Length 185;
Best Local Similarity 70.6%; Pred. No. 6.4e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 9
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match      67.7%; Score 136; DB 4; Length 185;
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Best Local Similarity 70.6%; Pred. No. 6.4e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 10
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 67.7%; Score 136; DB 4; Length 281;
Best Local Similarity 70.6%; Pred. No. 9.6e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 11
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 46.5%; Score 93.5; DB 4; Length 117;
Best Local Similarity 65.7%; Pred. No. 0.00044;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

Qy 2 SQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27
```

```
RESULT 12
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match 33.1%; Score 66.5; DB 4; Length 59;
Best Local Similarity 32.4%; Pred. No. 0.35;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 33

RESULT 13
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match 33.1%; Score 66.5; DB 4; Length 67;
Best Local Similarity 32.4%; Pred. No. 0.4;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CPEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 33

RESULT 14
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
```



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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

;
; 1 CSQNEVFDLSLHACIPQCLRCSSNTPLTCQRYC 34
; : : : : : : : : : : : : : : : :
; 34 CPPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC 66

RESULT 20
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
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;
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match 33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

;
; 1 CSQNEVFDLSLHACIPQCLRCSSNTPLTCQRYC 34
; : : : : : : : : : : : : : : : :
; 34 CPPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC 66

RESULT 21
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; TYPE: PRT
; LENGTH: 293
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

;
; 1 CSQNEVFDLSLHACIPQCLRCSSNTPLTCQRYC 34
; : : : : : : : : : : : : : : : :
; 34 CPPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC 66

RESULT 22
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; THEREON
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC 66

RESULT 23
US-09-854-864-14
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC 66

RESULT 24
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match      33.1%; Score 66.5; DB 4; Length 397;
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Best Local Similarity 32.4%; Pred. No. 2.2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-ORTCAAFC 66

RESULT 25
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,967
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-967-2

Query Match      27.9%; Score 56; DB 2; Length 2476;
Best Local Similarity 31.8%; Pred. No. 2.3e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSQNEYFDSLHACIP-CQ---LRCSNTPPLTCQRYC 34
Db 1851 CSAHSVYTSVPSCLPSCQDPGQCTGAGAPSTCEGC 1888

RESULT 26
US-09-621-976-6330
; Sequence 6330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
```


US-09-848-295-2

Query Match 26.1%; Score 52.5; DB 4; Length 142;
Best Local Similarity 29.4%; Pred. No. 37;
Matches 10; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

Qy 1 CSQNEYFSLHACIPCOLRCSSNTPPLTCQRYC 34
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 4 CPEQYWAALLGTCMFCKAICNHQS-QRTCAASC 36

RESULT 31

US-09-877-730-26
; Sequence 26, Application US/09877730
; Patent No. 6465632

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro

; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the

; FILE REFERENCE: LEX-0189-USA

; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26
; LENGTH: 547

; TYPE: PRT
; ORGANISM: homo sapiens

US-09-877-730-26

Query Match 25.9%; Score 52; DB 4; Length 547;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYFDSLHACIPCOLRCSSNTPPLTCQRY 33
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 503 NSFIDAKVLSGICISRSISPPPCVCKMY 532

RESULT 32

US-09-877-730-24

; Sequence 24, Application US/09877730
; Patent No. 6465832

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro

; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the

; FILE REFERENCE: LEX-0189-USA

; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24
; LENGTH: 624

; TYPE: PRT
; ORGANISM: homo sapiens

US-09-877-730-24

Query Match 25.9%; Score 52; DB 4; Length 624;

Best Local Similarity 33.3%; Pred. No. 1.8e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYFDSLHACIPCOLRCSSNTPPLTCQRY 33
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 580 NSFIDAKVLSGICISRSISPPPCVCKMY 609

RESULT 33

US-09-877-730-22

; Sequence 22, Application US/09877730
; Patent No. 6465632

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro

; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the

; FILE REFERENCE: LEX-0189-USA

; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22
; LENGTH: 712

; TYPE: PRT
; ORGANISM: homo sapiens

US-09-877-730-22

Query Match 25.9%; Score 52; DB 4; Length 712;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 4 NEYFDSLHACIPCOLRCSSNTPPLTCQRY 33
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 668 NSFIDAKVLSGICISRSISPPPCVCKMY 697

RESULT 34

US-09-877-730-16

; Sequence 16, Application US/09877730
; Patent No. 6465632

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro

; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the

; FILE REFERENCE: LEX-0189-USA

; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16
; LENGTH: 826

; TYPE: PRT
; ORGANISM: homo sapiens

US-09-877-730-16

Query Match 25.9%; Score 52; DB 4; Length 826;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 4 NEYFDSLHACIPQLRCSNTPPLTCQRY 33
 | : | : | : | : | : | : | : |
Db 782 NSFIDAKVLSCGICCISSRSIPIPPCVCKMY 811

```

RESULT 35
US-09-877-730-6
; Sequence 6, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-6

```

```

RESULT 36
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich; Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877, 730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 991
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12

```

```

RESULT 37
US-09-877-730-2
; Sequence 2, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Poly
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 2001-06-09
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2

```

RESULT 38
US-08-117-080-12
Sequence 12, Application US/08117080
Patent No. 5482928
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,080
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-117-080-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSSNT-PPLTCQRYC 34
Db 24 MIEACIINGRCNENVGPPYCCSGFC 49

RESULT 39

US-08-471-329-12
Sequence 12, Application US/08471329
Patent No. 5889048
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,329
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-471-329-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;
Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSSNT-PPLTCQRYC 34
Db 24 MIEACIINGRCNENVGPPYCCSGFC 49

RESULT 40

US-08-915-142-12
Sequence 12, Application US/08915142
Patent No. 5942663
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROEKAERT, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,142
FILING DATE: 20-APR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,329
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELEPHONE: (202) 861 3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
US-08-915-142-12

Query Match 25.6%; Score 51.5; DB 2; Length 63;
Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
Qy 10 LLHACIPQLRCSSNT-PLTCQRYC 34
Db 24 MIEACIGNGRGNVGVPPYCCSGFC 49

RESULT 41

US-08-465-380-4
; Sequence 4, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD----CGTKPCPEAKCNPEPPPEEDPICRSRG 42

RESULT 42

US-08-465-380-40

; Sequence 40, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD----CGTKPCPEAKCNPEPPPEEDPICRSRG 42

RESULT 43

US-08-480-478-33
; Sequence 33, Application US/08480478
; Patent No. 5864009
; GENERAL INFORMATION:
; APPLICANT: GEORGE P. VLASUK; PATRICK ERIC

; APPLICANT: HUGO STANSSENS; JORIS HILDA
; APPLICANT: LIEVEN MESSENS; MARC JOZEF
; APPLICANT: LAUMEREYS; YVES RENE LAROCHE;
; APPLICANT: LAURENT STEPHANE JESPEERS; and
; APPLICANT: YANNICK GEORGES JOZEF
; APPLICANT: GANSEMANS
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
; COAGULANT PROTEIN

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-397-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD-----CGTQKPCCAKCNBPPEEDPICRSRG 42

RESULT 46

US-08-486-399-4
Sequence 4, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-399-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD-----CGTQKPCCAKCNBPPEEDPICRSRG 42

RESULT 47

US-08-486-399-40
Sequence 40, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-399-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSONEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34
Db 6 CGENEWLDD-----CGTQKPCCAKCNBPPEEDPICRSRG 42

RESULT 48

US-08-486-965-4

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RESULT 49
US-08-461-965-40
; Sequence 40, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.-J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:

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RESULT 50

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,110A
; FILING DATE: 18 OCTOBER 1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 208/290
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-326-110A-33

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSQNEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 CGENEWLDD---CGTQKPCPEAKCNEEPPEEDPICRSGC 42
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Search completed: January 28, 2005, 19:48:41
Job time : 11.0459 secs

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